

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 19:32:18 ; Search time 1486.5 Seconds
(without alignments)
6298.931 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaagcagcatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	198	100.0	1588	6	AR263641	AR263641 Sequence
2	198	100.0	1659	6	E31042	E31042 Method for
3	198	100.0	1659	6	AR270490	AR270490 Sequence
4	198	100.0	1659	9	HSU32974	U32974 Human IAP-1
5	198	100.0	2086	9	BC032729	BC032729 Homo sapi
6	198	100.0	2404	6	CQ714226	CQ714226 Sequence
7	198	100.0	2404	6	AX429575	AX429575 Sequence
8	198	100.0	2540	6	AR103281	AR103281 Sequence
9	198	100.0	2540	6	CQ789350	CQ789350 Sequence
10	198	100.0	2540	6	AR302736	AR302736 Sequence
11	198	100.0	2540	6	AR380355	AR380355 Sequence
12	198	100.0	2540	6	AR435471	AR435471 Sequence
13	198	100.0	2540	6	AR451571	AR451571 Sequence
14	198	100.0	2540	6	AR473581	AR473581 Sequence
15	198	100.0	2540	6	AX412118	AX412118 Sequence
16	198	100.0	2540	6	AX587804	AX587804 Sequence
17	198	100.0	2540	9	HSU45880	U45880 Human X-lin
18	198	100.0	3000	6	AR451578	AR451578 Sequence
19	198	100.0	3000	6	AX412131	AX412131 Sequence

20	198	100.0	5232	6	AR106397	AR106397 Sequence
21	198	100.0	5232	6	AR116699	AR116699 Sequence
22	198	100.0	5232	6	BD190868	BD190868 Detection
23	198	100.0	5232	6	AR370617	AR370617 Sequence
24	198	100.0	5232	6	AX670900	AX670900 Sequence
25	180.4	91.1	1088	6	CQ734077	CQ734077 Sequence
26	180.4	91.1	1752	6	AX104956	AX104956 Sequence
27	180.4	91.1	1752	9	AF164681	AF164681 Homo sapi
28	180.4	91.1	154214	9	AC079753	AC079753 Homo sapi
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30	179.4	90.6	2468	10	AB033366	AB033366 Rattus no
31	179.4	90.6	3032	10	AF304334	AF304334 Rattus no
32	177.8	89.8	2032	10	AF304333	AF304333 Rattus no
33	174.6	88.2	1988	10	MMU36842	U36842 Mus musculu
34	173	87.4	2100	6	AR302739	AR302739 Sequence
35	173	87.4	2100	6	AR435474	AR435474 Sequence
36	173	87.4	2100	6	AR451574	AR451574 Sequence
37	173	87.4	2100	6	AR473584	AR473584 Sequence
38	173	87.4	2100	6	AX412124	AX412124 Sequence
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42	169.8	85.8	2691	6	AR370620	AR370620 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AR263641 1588 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 3 from patent US 6331412.
ACCESSION AR263641
VERSION AR263641.1 GI:28075567
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1588)
AUTHORS Korneluk,R.G. and Lagace,M.
TITLE Methods and compounds for modulating male fertility
JOURNAL Patent: US 6331412-A 3 18-DEC-2001;
FEATURES Location/Qualifiers
source 1..1588
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 198; DB 6; Length 1588;
Best Local Similarity 100.0%; Pred. No. 2.8e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||
886 GCAAGAGCTGGATTTTATGCTTTTAGTGTAAGTGATAAGTAAAGTGTCTTCACTGTGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGGAGACCCCTTGGGAACAACATGCTAAATGCTAT 180
DB |||||
946 GGAGGGCTAACTGATTGGAAGCCAGTGGAGACCCCTTGGGAACAACATGCTAAATGCTAT 1005
QY 181 CCAGGGTCAAAATATCTG 198
DB |||||
1006 CCAGGGTCAAAATATCTG 1023
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.8e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 CCAGGTCGAATATCTG 198
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DB 1054 CCAGGTCGAATATCTG 1071
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RESULT 5

BC032729
LOCUS
DEFINITION Homo sapiens baculoviral IAP repeat-containing 4, mRNA (cDNA clone
MGC:45369 IMAGE:5532247), complete cds.
ACCESSION BC032729.1 GI:21619763
VERSION
KEYWORDS
SOURCE MGC.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2086)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.P., Jordan,H., Moore,T., Max,A.M., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheet,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
Abramson,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Faney,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2086)
Strausberg,R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian

TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nih.gov

Akhter,N., Ayelle,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 69 Row: j Column: 18

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 4502142.

Location/Qualifiers

1..2086

FEATURES

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/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

1..2086

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/note="synonyms: MIHA, ILP1, API3, XIAP"

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79..1572

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/db_xref="LocusID:331"

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ORIGIN

Query Match 100.0%; Score 198; DB 9; Length 2086;
Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTGGACATGATATCTACGTAAACAGGAGCAGCTT 60
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QY 61 GCAAGAGCTGGATTTATGCTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 120
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DB 931 GCAAGAGCTGGATTTATGCTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 990
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TITLE
JOURNAL
transgenic drosophila melanogaster expressing beta amyloid
Patent: WO 0226820-A 38 04-APR-2002;
NOVARTIS ERFIND VERWALT GMBH (AT)


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ACCESSION      CQ789350
VERSION        CQ789350.1 GI:45822921
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1
AUTHORS        Kroenke,M., Kashkar,H., Hamilton-Dutoit,S.J. and Juergensmeier,J.M.
TITLE          USE OF IAP FOR THE DIAGNOSIS AND OF IAP-INHIBITORS FOR THE
JOURNAL        TREATMENT OF HDGKINERQUO;S LYMPHOMAS
PATENT         Patent: WO 2004/017991-A 1 04-MAR-2004;
CELL           Cell Center Cologne GmbH (DE)
FEATURES       Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB   886 GCAAGAGCTGGATTATTCCTTTTAGGTGAAGTGATAAAGTAAGTGTCTTTCACTGTGGA 945

QY   121  GGAGGGCTAACCTGATTGGAGCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180
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QY   181  CCAGGGTGC AAATATCTG 198
DB   1006 CCAGGGTGC AAATATCTG 1023

RESULT 11
LOCUS      AR380355
DEFINITION Sequence 900 from patent US 6607879.
ACCESSION  AR380355
VERSION    AR380355.1 GI:40087989
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 2540)
AUTHORS    Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE      Compositions for the detection of blood cell and immunological response gene expression
JOURNAL    Patent: US 6607879-A 900 19-AUG-2003;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.7e-44;
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QY   61   GCAAGAGCTGGATTATTCCTTTTAGGTGAAGTGATAAAGTAAGTGTCTTTCACTGTGGA 120
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DB   1006 CCAGGGTGC AAATATCTG 1023

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LOCUS      AR435471
DEFINITION Sequence 3 from patent US 6656704.
ACCESSION  AR435471
VERSION    AR435471.1 GI:40198322
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 2540)
AUTHORS    Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE      Mammalian IAP gene family, primers, probes and detection methods
JOURNAL    Patent: US 6541457-A 3 01-APR-2003;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 3 from patent US 6541457.
ACCESSION  AR302736
VERSION    AR302736.1 GI:31691179
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 2540)
AUTHORS    Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE      Mammalian IAP gene family, primers, probes and detection methods
JOURNAL    Patent: US 6541457-A 3 01-APR-2003;
FEATURES   Location/Qualifiers
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ORIGIN

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ACCESSION      CQ789350
VERSION        CQ789350.1 GI:45822921
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1
AUTHORS        Kroenke,M., Kashkar,H., Hamilton-Dutoit,S.J. and Juergensmeier,J.M.
TITLE          USE OF IAP FOR THE DIAGNOSIS AND OF IAP-INHIBITORS FOR THE TREATMENT OF HDGKINERQUO;S LYMPHOMAS
JOURNAL        Patent: WO 2004/017991-A 1 04-MAR-2004; Cell Center Cologne GmbH (DE)
FEATURES       Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   181 CCAGGGTCAAATATCTG 198
DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   1006 CCAGGGTCAAATATCTG 1023

RESULT 11
LOCUS           AR380355
DEFINITION     Sequence 900 from patent US 6607879.
ACCESSION      AR380355
VERSION        AR380355.1 GI:40087989
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 2540)
AUTHORS        Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE          Compositions for the detection of blood cell and immunological response gene expression
JOURNAL        Patent: US 6607879-A 900 19-AUG-2003;
FEATURES       Location/Qualifiers
               1..2540
               /organism="unknown"
               /mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   1006 CCAGGGTCAAATATCTG 1023

RESULT 12
LOCUS           AR435471
DEFINITION     Sequence 3 from patent US 6656704.
ACCESSION      AR435471
VERSION        AR435471.1 GI:40198322
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 2540)
AUTHORS        Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE          Mammalian IAP gene family, primers, probes and detection methods
JOURNAL        Patent: US 6541457-A 3 01-APR-2003;
FEATURES       Location/Qualifiers
               1..2540
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ORIGIN
Query Match      100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1  TATGAAGCACCGATCTTTACTTTTGGACATGATATACTCAGTTAACAGGACGACTT 60
DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   1006 CCAGGGTCAAATATCTG 1023

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LOCUS           AR302736
DEFINITION     Sequence 3 from patent US 6541457.
ACCESSION      AR302736
VERSION        AR302736.1 GI:31691179
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 2540)
AUTHORS        Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE          Mammalian IAP gene family, primers, probes and detection methods
JOURNAL        Patent: US 6541457-A 3 01-APR-2003;
FEATURES       Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY   61  GCAAGAGCTGGATTATTCCTTTAGGTGAAGTGATAAAGTAAAGTGCCTTCACTGTGGA 120
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QY   121 GGAGGCTTAAGTATTGGAAGCCAGTGAAGACCCTTCGGGAACAACATGCTAAATGGTAT 180
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QY   181 CCAGGGTCAAATATCTG 198
DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   1006 CCAGGGTCAAATATCTG 1023

RESULT 10
LOCUS           AR302736
DEFINITION     Sequence 3 from patent US 6541457.
ACCESSION      AR302736
VERSION        AR302736.1 GI:31691179
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 2540)
AUTHORS        Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE          Mammalian IAP gene family, primers, probes and detection methods
JOURNAL        Patent: US 6541457-A 3 01-APR-2003;
FEATURES       Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY   181 CCAGGGTCAAATATCTG 198
DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 10
LOCUS           AR302736
DEFINITION     Sequence 3 from patent US 6541457.
ACCESSION      AR302736
VERSION        AR302736.1 GI:31691179
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 2540)
AUTHORS        Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE          Mammalian IAP gene family, primers, probes and detection methods
JOURNAL        Patent: US 6541457-A 3 01-APR-2003;
FEATURES       Location/Qualifiers
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               /organism="unknown"

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Query Match      100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY   181 CCAGGGTCAAATATCTG 198
DB   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   1006 CCAGGGTCAAATATCTG 1023

RESULT 10
LOCUS           AR302736
DEFINITION     Sequence 3 from patent US 6541457.
ACCESSION      AR302736
VERSION        AR302736.1 GI:31691179
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 2540)
AUTHORS        Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE          Mammalian IAP gene family, primers, probes and detection methods
J
```

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2540)
TITLE	Korneluk,R.G., Mackenzie,A.E., Baird,S. and Liston,P.
JOURNAL	Mammalian apoptosis inhibitor protein gene family, primers, probes and detection methods
FEATURES	Patent: US 6656704-A 3 02-DEC-2003;
source	Location/Qualifiers
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Query Match	100.0%; Score 198; DB 6; Length 2540;
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QY	61 GCAAGAGCTGGATTATTCGTCTTAGGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 120
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QY	886 GCAAGAGCTGGATTATTCGTCTTAGGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 945
DB	
QY	121 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGCCCTTTGGGAACACATGCTTAATGGTAT 180
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QY	946 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGCCCTTTGGGAACACATGCTTAATGGTAT 180
DB	
QY	181 CCAGGGTGCAAATATCTG 198
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LOCUS	Sequence 218 from patent US 6673917.
DEFINITION	AR451571
ACCESSION	AR451571
VERSION	AR451571.1 GI:42682596
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2540)
TITLE	Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
JOURNAL	Antisense IAP nucleic acids and uses thereof
FEATURES	Patent: US 6673917-A 218 06-JAN-2004;
source	Location/Qualifiers
	1..2540
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Best Local Similarity	100.0%; Pred.No.2.7e-44;
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DB	
QY	61 GCAAGAGCTGGATTATTCGTCTTAGGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 120
DB	
QY	886 GCAAGAGCTGGATTATTCGTCTTAGGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 945
DB	
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DB	
QY	946 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGCCCTTTGGGAACACATGCTTAATGGTAT 180
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QY	121	GGAGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT	180
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QY	181	CCAGGTCGAATATCTG	198
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
3982.319 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaagcagcatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	198	100.0	1588	6	ABSS2803 DNA encod
2	198	100.0	1659	3	Aaz48862 Human XIA
3	198	100.0	1659	10	ACA56455 Human sig
4	198	100.0	1659	12	ADI56251 Human pol
5	198	100.0	2404	6	AAK99405 DNA of Ap
6	198	100.0	2540	2	Aat70836 Human apo
7	198	100.0	2540	3	AAa64901 Human X-1
8	198	100.0	2540	6	ABK93869 Human cDN
9	198	100.0	2540	6	ABV94283 Breast ca
10	198	100.0	2540	8	AAI53731 X-linked
11	198	100.0	2540	8	AAa49663 Human X-1
12	198	100.0	2540	9	ADb81002 RING-SH c
13	198	100.0	2540	10	ADG89383 Cancer de
14	198	100.0	2540	11	ADI31574 Human cDN
15	198	100.0	2540	12	ADH74638 DNA encod
16	198	100.0	2540	12	ADL70165 Human X c
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18	198	100.0	5232	2	AAV55038 Human XIA
19	180.4	91.1	1752	4	AAAD03575 Human IAP
20	174.6	88.2	1988	2	AAT72710 Mouse inh
21	173	87.4	2100	2	AAT70839 Mouse apo

22	173	87.4	2100	6	ABK93872 Mouse cDN
23	169.8	85.8	2691	2	AAV55041 Murine XI
24	169.8	85.8	2691	8	ABZ58102 Mouse inh
25	166	83.8	711	4	AAAD03582 Chimpanze
26	166	83.8	1758	6	ABK14678 Human Inh
27	166	83.8	1758	6	ABK14677 Human Inh
28	166	83.8	4393	4	AAAD03581 Human IAP
29	164.4	83.0	711	3	AAA06940 DNA encod
30	164.4	83.0	1559	6	ABK13137 Human tes
31	164.4	83.0	1559	6	ABSS2802 DNA encod
32	162.8	82.2	711	4	AAAD03583 Gorilla I
33	157.8	79.7	578	2	AAAX02960 Human IL-
34	131.4	66.4	802	2	AAAX03018 Human IL-
35	96.8	48.9	302	6	ABQ58785 Human col
36	83	41.9	1402	2	AAAX03028 Human IL-
37	78.6	39.7	1448	12	ADQ26591 cDNA enco
38	78.6	39.7	2563	9	ADb80989 RING-SH c
39	78.6	39.7	2563	10	ACA56478 Human sig
40	78.6	39.7	2563	11	ADI31568 Human cDN
41	78.6	39.7	2563	12	ADI56274 Human pol
42	78.6	39.7	2601	2	AAT761591 Human c-I
43	78.6	39.7	2666	2	AAT70837 Human apo
44	78.6	39.7	2676	6	ABK93870 Human cDN
45	78.6	39.7	2916	12	ADF45449 Human vas

ALIGNMENTS

RESULT 1

ABSS2803
ID ABSS2803 standard; DNA; 1588 BP.

XX AC ABSS2803;

XX DT 15-NOV-2002 (first entry)

XX DE DNA encoding X-linked inhibitor of apoptosis, XIAP.

XX KW Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; TIAP;

XX KW fertility; testicular cancer; male infertility; male birth control;

XX KW X-linked inhibitor of apoptosis; gene; ds.

XX OS Mammalia.

XX FH Key Location/Qualifiers

FT CDS 34..1527

FT /*tag= a

FT /transl_except= (pos:34..36, aa:Xaa)

FT /product= "X-linked inhibitor of apoptosis protein, XIAP"

FT /partial

FT /note= "Start codon illegible in specification;

FT represented as nnn"

XX US2002086409-A1.

XX PD 04-JUL-2002.

XX PF 18-DEC-2001; 2001US-00024433.

XX PR 29-JAN-1998; 98US-0073001P.

XX PR 29-JAN-1999; 99US-00239867.

XX PA (KORN/) KORNELUK R G.

XX PA (LAGA/) LAGACE M.

XX PI Korneluk RG, Lagace M;

XX DR WPI; 2002-642245/69.

XX DR P-PSDB; ABG32418.

XX PT Novel polypeptide, a member of apoptosis family of proteins that is expressed in testes useful for modulating apoptosis in cells,

PT particular cells involved in male fertility.
 XX
 PS Example 3; Fig 4A; 24pp; English.
 XX
 CC A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
 CC apoptosis) family of proteins that is expressed in the testes. (I) is
 CC useful for identifying a compound that modulates TIAP biological activity
 CC (I) is useful for increasing apoptosis in a cell, preferably a germ-line
 CC cell and for increasing fertility in an animal. (I) is useful for
 CC treating or preventing apoptosis which occurs as a part of testicular
 CC cancer and male infertility. TIAP may be manipulated for use as a male
 CC birth control. TIAP polypeptides and nucleic acid sequences also have
 CC diagnostic use in the detection or monitoring of conditions involving
 CC aberrant levels of apoptosis. The present sequence represents the coding
 CC sequence of X-linked inhibitor of apoptosis (XIAP)
 XX
 SQ Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;
 Query Match 100.0%; Score 198; DB 6; Length 1588;
 Best Local Similarity 100.0%; Pred. No. 3.8e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAAGGAGCAGCTT 60
 DB 826 TATGAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAAGGAGCAGCTT 885
 QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 120
 DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 945
 QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 DB 946 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
 QY 181 CCAGGGTGCAAAATATCTG 198
 DB 1006 CCAGGGTGCAAAATATCTG 1023
 RESULT 2
 AAZ48862
 ID AAZ48862 standard; cdna; 1659 BP.
 XX
 AC AAZ48862;
 XX
 DT 24-MAR-2000 (first entry)
 XX
 DE Human XIAP coding sequence.
 XX
 KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KW transforming growth factor-beta activated kinase 1; monocyte migration;
 KW TAK1 binding protein 1; extracellular matrix protein production;
 KW cell growth inhibitor; beta-amyloid protein deposition;
 KW immunosuppression; Transforming growth factor-beta; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP11326328-A.
 XX
 PD 26-NOV-1999.
 XX
 PF 13-MAY-1998; 98JP-00130378.
 XX
 PR 13-MAY-1998; 98JP-00130378.
 XX
 PA (MATS/) MATSUMOTO K.
 XX
 DR WPI; 2000-078337/07.
 DR P-PSDB; AAY59451.
 XX
 PT Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein.
 XX
 PS Disclosure; Page 28-30; 43pp; Japanese.
 XX
 CC This sequence encodes the human XIAP protein. The invention relates to a
 CC method for screening a substance inhibiting the formation of a complex
 CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
 CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
 CC protein 1 (TAB1) and a substance to be tested are contacted with each
 CC other and then the presence or formation of a complex between XIAP and
 CC TAB1 is detected. The substance can be used as a drug for extracellular
 CC matrix protein production enhancement, cell growth inhibition, monocyte
 CC migration, physiologically active substance induction, immunosuppression,
 CC and beta-amyloid protein deposition. A substance inhibiting the formation
 CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
 CC (Transforming growth factor-beta) type I and/or type II receptor is
 CC useful as a drug
 XX
 SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 3; Length 1659;
 Best Local Similarity 100.0%; Pred. No. 3.9e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAAGGAGCAGCTT 60
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 QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 120
 DB 934 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 993
 QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 DB 994 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053
 QY 181 CCAGGGTGCAAAATATCTG 198
 DB 1054 CCAGGGTGCAAAATATCTG 1071
 RESULT 3
 ACA56455
 ID ACA56455 standard; cdna; 1659 BP.
 XX
 AC ACA56455;
 XX
 DT 06-JUN-2003 (first entry)
 XX
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1053.
 XX
 KW Human; probe; ss; array element; Parkinson's disease;
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 XX
 OS Homo sapiens.
 XX
 PN US6500938-B1.
 XX
 PD 31-DEC-2002.
 XX
 PF 30-JAN-1998; 98US-00016434.
 XX
 PR 30-JAN-1998; 98US-00016434.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Seilhamer JU;
 XX
 DR WPI; 2003-352189/33.
 XX
 PT Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PT polynucleotides.
 XX

PS Claim 1; SEQ ID NO 1053; 65pp; English.

XX The invention relates to a combination which, comprises a number of

CC polynucleotide probes comprising a sequence selected from one of the 1490

CC sequences mentioned in the specification. The combination is useful as an

CC array element in a microarray for monitoring the expression of a number

CC of target polynucleotides. The microarray is particularly useful in the

CC diagnosis and treatment of cancer and immunopathology and neuropathology.

CC The microarray is useful in diagnostics and treatment regimens, drug

CC discovery and development, toxicological and carcinogenicity studies,

CC forensics and pharmacogenomics. The microarray is also useful for

CC monitoring progression of diseases and for developing sophisticated

CC profiles for the effects of currently available therapeutic drugs. The

CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs

CC and genomic fragments and in research and diagnostic applications. The

CC array can detect changes in expression in a large number of genes coding

CC for different signalling pathway populations which can be used to diagnose

CC various diseases including cancer e.g. adenocarcinoma and leukaemia,

CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease

CC and Parkinson's disease. The present sequence represents a polynucleotide

CC probe of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic

CC format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=06500938B1

XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 198; DB 10; Length 1659;

Best Local Similarity 100.0%; Pred. No. 3.9e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 874 TATGAGCAGCGATCTTTACTTTTGGACATGATATCTCAGTTAAAGTAAAGTCTTCACTGTGGA 933

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGAATGATTAAGTCTTCACTGTGGA 120

DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGAATGATTAAGTCTTCACTGTGGA 993

QY 121 GGAGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180

DB 994 GGAGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053

QY 181 CCAGGCTGCAATATCTG 198

DB 1054 CCAGGCTGCAATATCTG 1071

RESULT 4

ID ADI56251

AC ADI56251 standard; DNA; 1659 BP.

XX ADI56251;

XX 22-APR-2004 (first entry)

XX Human polynucleotide probe #1053.

XX Human; probe; ss; receptor-like polypeptide; transducing polypeptide;

KW effector-like polypeptide; cancer; immunopathology; neuropathology;

KW drug development; toxicology; carcinogenicity;

KW signalling pathway polypeptide; adrenal gland; bladder; bone;

KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;

KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;

KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.

XX Homo sapiens.

OS AAK99405

EN AAK99405 standard; DNA; 2404 BP.

XX AAK99405;

XX 15-JAN-2004.

PD 26-NOV-2002; 2002US-00305720.

PF

XX PR 30-JAN-1998; 98US-00016434.

XX (INCY-) INCYTE GENOMICS INC.

XX Au-Young J, Seilhamer JJ;

XX WPI; 2004-090520/09.

PT New composition comprising polynucleotide probes, useful as array

PT elements in a microarray for monitoring the expression of target

PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic

PT fragments.

XX Claim 6; SEQ ID NO 1053; 73pp; English.

XX The invention relates to a composition of polynucleotide probes

CC comprising first polynucleotide probes comprising at least a portion of a

CC gene encoding a receptor-like polypeptide, second polynucleotide probes

CC comprising at least a portion of a gene encoding a transducing

CC polypeptide and third polynucleotide probes comprising at least a portion

CC of a gene encoding an effector-like polypeptide. The probes of the

CC composition are useful as array elements in a microarray for monitoring

CC the expression of target polynucleotides. The microarray is useful in the

CC diagnosis and treatment of cancer, an immunopathology or a

CC neuropathology. It can also be used for drug discovery and development,

CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.

CC Microarrays can also be used for monitoring the progression of diseases

CC that may be associated with the altered expression of signalling pathway

CC polypeptides. The composition can also be used to purify a subpopulation

CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile

CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of

CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,

CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or

CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,

CC epilepsy, Alzheimer's disease or depression. This sequence represents a

CC human polynucleotide probe of the invention. Note: The sequence data for

CC this patent did not form part of the printed specification but was

CC obtained in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html.

XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 198; DB 12; Length 1659;

Best Local Similarity 100.0%; Pred. No. 3.9e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTTACTTTTGGACATGATATCTCAGTTAAAGTAAAGTCTTCACTGTGGA 60

DB 874 TATGAGCAGCGATCTTTACTTTTGGACATGATATCTCAGTTAAAGTAAAGTCTTCACTGTGGA 933

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGAATGATTAAGTCTTCACTGTGGA 120

DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGAATGATTAAGTCTTCACTGTGGA 993

QY 121 GGAGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180

DB 994 GGAGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053

QY 181 CCAGGCTGCAATATCTG 198

DB 1054 CCAGGCTGCAATATCTG 1071

RESULT 5

AAK99405

ID AAK99405 standard; DNA; 2404 BP.

XX AAK99405;

XX 27-JUN-2002 (first entry)

XX DNA of APP related human homologue hCF35211.

XX Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 692..1528
FT /*tag= a
FT /product= "Protein of human homologue hCP35211"
FT /note= "No start codon"

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-EP011345.

XX 29-SEP-2000; 2000US-0236893P.

XX 14-JUN-2001; 2001US-0298309P.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;

XX Reinhardt MWM, Zusman S;

XX WPI; 2002-315796/35.

XX P-PSDB; AA020511.

XX New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease.

XX Example 4; Page 111; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC represents the DNA of the APP related human homologue hCP35211

XX Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 6; Length 2404;
Best Local Similarity 100.0%; Pred. No. 4.4e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTTGGACATGATATCTCAGTTAAACAGGAGCAGCTT 60
Db 827 TATGAAGCAGGATCTTTTGGACATGATATCTCAGTTAAACAGGAGCAGCTT 886

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120
Db 887 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 946

QY 121 GGAGGGCTAACTGATTGGAGCCCACTGAGAGCCCTTTGGGAACAACATGCTAAATGCTAT 180
Db 947 GGAGGGCTAACTGATTGGAGCCCACTGAGAGCCCTTTGGGAACAACATGCTAAATGCTAT 1006

QY 181 CCAGGGTGCAATATCTG 198

Db 1007 CCAGGGTGCAATATCTG 1024

RESULT 6

AAT70836

ID AAT70836 standard; cDNA; 2540 BP.

XX AAT70836;

AC AAT70836;

XX 02-SEP-1997 (first entry)

XX Human apoptosis inhibitor xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 34..1527
FT /*tag= a

XX WO9706255-A2.

XX 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB001022.

XX 04-AUG-1995; 95US-00511485.

XX 22-DEC-1995; 95US-00576956.

XX (UYOI-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;

XX WPI; 1997-154262/14.

XX P-PSDB; AAW19581.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.

XX Claim 12; Page 67-68; 219pp; English.

XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2
CC genes (AAT70836-41) respectively code for a new class of mammalian
CC proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap
CC gene (for X-linked IAP gene) was isolated from a human foetal brain ZapII
CC cDNA library using an X-linked sequence tag site that shows strong
CC homology with the conserved ring zinc finger domain of baculovirus CpiAP
CC and OpiAP genes. The gene was assigned to chromosome Xq25 by FISH. IAP
CC nucleic acids can be used to express IAP polypeptides in cells and
CC animals to inhibit apoptosis, and as primers and probes to identify and
CC isolate additional IAP genes, as well as in methods for treating diseases
CC and disorders involving apoptosis (anti-apoptotic gene therapy)

XX Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;

Query Match 100.0%; Score 198; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTTGGACATGATATCTCAGTTAAACAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCTTTTGGACATGATATCTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAGCCCACTGAGAGCCCTTTGGGAACAACATGCTAAATGCTAT 180

Db 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCTTGGAAACACATGCTAAATGGTAT 1005
 QY 181 CCAGGTCGCAAAATATCTG 198
 Db 1006 CCAGGTCGCAAAATATCTG 1023
 RESULT 7
 AA64901
 ID AAA64901 standard; DNA; 2540 BP.
 AC AAA64901;
 DT 07-NOV-2000 (first entry)
 DE Human X-linked inhibitor of apoptosis DNA.
 KW X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880; antisense;
 KW antiinflammatory; cytostatic; tumour; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 34..1527
 FT /*tag= a
 FT /product= "X-linked inhibitor of apoptosis"
 XX
 FN US6087173-A.
 XX
 PD 11-JUL-2000.
 PF 09-SEP-1999; 99US-00392580.
 PR 09-SEP-1999; 99US-00392580.
 XX (ISIS-) ISIS PHARM INC.
 PA Bennett CF, Cowse LM, Ackermann EJ;
 PI WPI; 2000-498201/44.
 DR P-PSDB; AAY99985.
 XX
 PT Antisense compound useful for research reagents, diagnostics, prophylaxis
 PT and for treating disorders associated with X-linked inhibitor of
 PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
 XX
 PS Example 13; Col 43-48; 33pp; English.
 XX
 CC The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis. The
 CC present sequence is the X-linked inhibitor of apoptosis DNA. Modified
 CC phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are more
 CC effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated with
 CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 CC prophylactically to prevent infection, inflammation or tumour formation
 XX
 SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 3; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 4.5e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGGATCTTTACCTTTGGGACATGATATCTAGTTAAACAGGAGCAGCTT 60
 Db 826 TATGAAGCAGGATCTTTACCTTTGGGACATGATATCTAGTTAAACAGGAGCAGCTT 885
 QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAACTGCTTTCACTGTGGA 120
 Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAACTGCTTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCTTGGAAACACATGCTAAATGGTAT 180
 Db 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCTTGGAAACACATGCTAAATGGTAT 1005
 QY 181 CCAGGTCGCAAAATATCTG 198
 Db 1006 CCAGGTCGCAAAATATCTG 1023
 RESULT 8
 ABK93869
 ID ABK93869 standard; cDNA; 2540 BP.
 XX AC ABK93869;
 DT 26-AUG-2002 (first entry)
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.
 KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200226968-A2.
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI; 2002-479562/51.
 DR P-PSDB; ABG65663.
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 XX
 PS Disclosure; Fig 1; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence
 XX
 SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 0 U; 22 Other;
 Query Match 100.0%; Score 198; DB 6; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 4.5e-54;

	Matches	199;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TATGAAGCACGGATCTTTTACTTTTTGGGACATGGATATACTCAGTTAAACAAGGACAGCTT	60							
Dd	826	TATGAAGCACGGATCTTTTACTTTTTGGGACATGGATATACTCAGTTAAACAAGGACAGCTT	885							
Qy	61	GCAAGAGCTCGATTTTATGCTTTTAGTGGAAGGTGATAAAGTAAAGTCCTTTCACGTGGGA	120							
Dd	886	GCAAGAGCTCGATTTTATGCTTTTAGTGGAAGGTGATAAAGTAAAGTCCTTTCACGTGGGA	945							
Qy	121	GGAGGGGCTTAATGATTCGGAAGCCAGTGAAGACCCTTTGGGAAACAACATGCTAAATGCTAT	180							
Dd	946	GGAGGGGCTTAATGATTCGGAAGCCAGTGAAGACCCTTTGGGAAACAACATGCTAAATGCTAT	1005							
Qy	181	CCAGGGTGCAAATATCTG	198							
Dd	1006	CCAGGGTGCAAATATCTG	1023							

RESULT 9	
ABV94283	ABV94283 standard; cDNA; 2540 BP.
ID	ABV94283
XX	AC
XX	AC
XX	ABV94283;
XX	
XX	08-JAN-2003 (first entry)
DT	
XX	Breast carcinoma related nucleotide sequence SEQ ID NO:274.
XX	Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
DE	ss.
XX	
XX	Homo sapiens.
OS	
XX	WO200246467-A2.
XX	13-JUN-2002.
XX	
XX	07-DEC-2001; 2001WO-IB002811.
PF	
XX	
XX	08-DEC-2000; 2000US-0254090P.
PR	
PR	07-DEC-2001; 2001US-00007926.
XX	
XX	(IPSO-) IPSOGEN.
PA	
XX	Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
XX	
XX	WPI; 2002-619023/66.
XX	
XX	Novel polynucleotide library useful in molecular characterization of a
PT	carcinoma, comprising a pool of polynucleotide sequences or its
PT	subsequences which are either underexpressed or overexpressed in tumor
PT	cells.
XX	
XX	Claim 1; Page 289; 401pp; English.
PS	

CC	cell, differentiating a tumour with lymph nodes from a tumour without
CC	lymph nodes, differentiating antracycline-sensitive tumours from
CC	antracycline-insensitive tumours, and classifying good and poor prognosis
CC	primary breast tumours. (I) is useful for large-scale molecular
CC	characterisation of breast cancer that help in prediction, prognosis and
CC	cancer treatment, and for detecting differentially expressed genes that
CC	correlated with a cancer
XX	
SQ	Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
	Query Match 100.0%; Score 198; DB 6; Length 2540;
	Best Local Similarity 100.0%; Pred.No. 4.5e-54;
	Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 TATGAAGCAGCGATCTTTACTTTTGGACATGATATACTCAGTTAAACAAGGACGACTT 60
Dd	826 TATGAAGCAGCGATCTTTACTTTTGGACATGATATACTCAGTTAAACAAGGACGACTT 885
Qy	61 GCAAGAGCTGGATTTCGTTCAGTGTAAGTGATAAAGTGCTTTCACTGTGGA 120
Dd	886 GCAAGAGCTGGATTTCGTTCAGTGTAAGTGATAAAGTGCTTTCACTGTGGA 945
Qy	121 GAGGGGCTAACTGATTGGAAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
Dd	946 GGAAGGCTAACTGATTGGAAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1005
Qy	181 CCAGGGTGCAATATCTG 198
Dd	1006 CCAGGGTGCAATATCTG 1023
RESULT 10	
AAL53731	
ID	AAL53731 standard; RNA; 2540 BP.
AC	AAL53731;
XX	
DT	07-FEB-2003 (first entry)
XX	
DE	X-linked inhibitor of apoptosis protein SEQ ID No 25.
XX	
KW	Target RNA; target RNA:support-attached test compound; flow cytometry;
XN	mass spectrometry; high-throughput screening; RNA motif; ss.
OS	Homo sapiens.
XX	
PN	WO200283837-A1.
XX	
PD	24-OCT-2002.
XX	
Pf	11-APR-2002; 2002WO-US011758.
XX	
PR	11-APR-2001; 2001US-0282966P.
XX	
PA	(PTCT-) PTC THERAPEUTICS INC.
XX	
PI	Almstead NG;
XX	
DR	WPI; 2003-075534/07.
XX	
PT	Identifying a test compound that binds to a target RNA molecule by
PT	separating the detectably labeled target RNA:support-attached test
PT	compound complex from uncomplexed target RNA molecules and test compounds
PT	by flow cytometry.
XX	
PS	Example; Page 79-80; 131pp; English.
XX	
CC	The invention relates to a novel method for identifying a test compound
CC	that binds to a target RNA molecule comprising separating the detectably
CC	labeled target RNA:support-attached test compound complex from
CC	uncomplexed target RNA molecules and test compounds. The separating
CC	process is carried out by flow cytometry and determining a structure of
CC	the type of test compound of the RNA:support-attached test compound

PT or filoviruses.

XX Disclosure; Fig 75; 176pp; English.

XX

CC The invention relates to a novel isolated protein complex comprising a RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A, STAM2B, VHS-UIM, a GTPase, an E2 enzyme, tsgl01, a cullin, RING-SH, and a clathrin. The novel protein complex has virucide activity and can be used to treat disorders as part of a vaccine. The protein complex and composition are useful for detecting cells infected with a virus, for identifying agents having antiviral activity, and for treating viral disorders caused by retroviruses, rhadoviruses, or filoviruses. This polynucleotide represents a DNA sequence relating to a protein comprising the RING-SH complex of the invention.

XX

SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 9; Length 2540;

Best Local Similarity 100.0%; Pred. No. 4.5e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGATATATCTCAGTTAACAGGACGCTT 60

DB 826 TATGAAGCAGGATCTTTACTTTTGGGACATGATATATCTCAGTTAACAGGACGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 120

DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 180

DB 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGCTGCAATATCTG 198

DB 1006 CCAGGCTGCAATATCTG 1023

RESULT 13

ADG89383

ID ADG89383 standard; DNA; 2540 BP.

XX

AC ADG89383;

XX

DT 11-MAR-2004 (first entry)

XX

DE Cancer detection method related gene #46.

XX

DE ds; cancer; gene expression;

XX

KW estrogen receptor-positive invasive breast cancer.

XX

XX Homo sapiens.

OS

XX WO2003078662-A1.

PN

XX 25-SEP-2003.

XX

XX 12-MAR-2003; 2003WO-US007713.

PF

XX 13-MAR-2002; 2002US-0364890P.

PR

XX 18-SEP-2002; 2002US-0412049P.

PR

XX (GENO-) GENOMIC HEALTH INC.

PA

XX Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;

PI

XX WPI; 2003-767536/72.

XX

XX Predicting clinical outcome for a patient diagnosed with cancer comprises determining the expression level of one or more genes, and compared to the amount found in a reference cancer tissue set.

XX

PS Disclosure; SEQ ID NO 331; 198pp; English.

XX

CC The invention relates to a method of predicting clinical outcome for a patient diagnosed with cancer by determining the expression level of one or more genes, or their expression products, selected from p53BP2, cathepsin B, cathepsin L, Kif7/MiB1, and thymidine kinase in a cancer tissue obtained from the patient, normalized against control gene(s), and compared to the amount found in a reference cancer tissue set. The specification also discloses an array comprising polynucleotides hybridizing to the following genes: FOXM1, PRAME, Sc12, SKI5, CSGP1, Ki-67, GSTM1, CA9, PR, BBC3, NME1, SURV, XIAP, Chk2, CDC25B, IGF1R, RPS6KB1, Src, Chk1, ID1, EstR1, p27, CCNB1, XIAP, Chk2, CDC25B, IGF1R, AKO55699, PI3KC2A, TGFB3, BAG1, CYP3A4, EPCAM, VEGFC, pS2, hENT1, WISP1, HNF3A, NFKBp65, BRCA2, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IFIA, CDH1, HIF1, IGF1R, CTSS, Her2 and DIABLO, immobilized on a solid surface. The methods are useful for predicting clinical outcome for a patient diagnosed with cancer, classifying cancer, and predicting the likelihood of long-term survival of a breast cancer patient, or a patient diagnosed with invasive breast cancer or with estrogen receptor (ER)-positive invasive breast cancer. This sequence corresponds to a gene sequence whose expression is detected by the method of the invention.

XX

SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 10; Length 2540;

Best Local Similarity 100.0%; Pred. No. 4.5e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGATATATCTCAGTTAACAGGACGCTT 60

DB 826 TATGAAGCAGGATCTTTACTTTTGGGACATGATATATCTCAGTTAACAGGACGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 120

DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 180

DB 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGCTGCAATATCTG 198

DB 1006 CCAGGCTGCAATATCTG 1023

RESULT 14

ADI31574

ID ADI31574 standard; cDNA; 2540 BP.

XX

AC ADI31574;

XX

DT 17-JUN-2004 (first entry)

XX

XX Human cDNA #900.

DE

XX

XX Human; gene; ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hyperosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer; osteopathic; antiarthritic; antirheumatic; cytostatic.

OS

XX Homo sapiens.

XX

XX US6607879-B1.

PN

XX 19-AUG-2003.

PD

XX 09-FEB-1998; 98US-00023655.

PF

XX 09-FEB-1998; 98US-00023655.

PR

XX (INCY-) INCYTE CORP.

PA

XX

PI Cocks BG, Stuart SG, Seilhamer JU;
XX WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 900; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperosinophilia, irritable bowel syndrome, and in
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
Query Match 100.0%; Score 198; DB 11; Length 2540;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCGCTT 60
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAAGCCCTTGGGACCAACATGCTAAATGGTAT 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAAGCCCTTGGGACCAACATGCTAAATGGTAT 945
QY 121 GGAGGGCTAACTGATTTAGTGAAGCCCTTGGGACCAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTTAGTGAAGCCCTTGGGACCAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTCAAAATATCTG 198
DB 1006 CCAGGGTCAAAATATCTG 1023
RESULT 15
ADH74638
ID ADH74638 standard; DNA; 2540 BP.
XX
AC ADH74638;
XX
DT 15-APR-2004 (first entry)
XX
DE DNA encoding human XIAP.
XX
KW Biomarker; prostate neoplastic condition; inhibitor of apoptosis; IAP;

KW XIAP; X chromosome-linked inhibitor of apoptosis; CIAP1; CIAP2;
KW prostate cancer; human; gene; ds.
XX
OS Homo sapiens.
XX
PN US2003224399-A1.
XX
PD 04-DEC-2003.
XX
XX 12-FEB-2003; 2003US-00366307.
XX
PR 12-FEB-2002; 2002US-0356956P.
XX
PA (REED/) REED J C.
XX (KRAJ/) KRAJEWSKI S.
XX
PI Reed JC, Krajewski S;
XX WPI; 2004-141816/14.
DR P-PSDB; ADH74639.
XX
PT Identifying biomarker that is diagnostic for survival of a patient with
PT prostate neoplastic condition by measuring level of integrin associated
PT protein in sample, and identifying correlation of the level in sample.
XX
PS Disclosure; SEQ ID NO 1; 42pp; English.
XX
CC The present invention relates to a method for identifying a biomarker
CC that is diagnostic for the survival of patient with a prostate neoplastic
CC condition. The method comprises measuring the level of inhibitor of
CC apoptosis (IAP) polypeptide chosen from chosen from XIAP (X chromosome-
CC linked inhibitor of apoptosis), CIAP1 and CIAP2 in a neoplastic prostate
CC cell-containing sample from patients, and identifying correlation between
CC the level of IAPs in the sample, where the correlation of an IAP with
CC survival in the patients indicates IAP as a biomarker diagnostic. The
CC method is useful for the prognosis of prostate neoplastic conditions such
CC as prostate cancer. The method is efficient in determining the prognosis
CC while the patient is still at an early stage of disease, and in
CC monitoring the effectiveness of a particular treatment in a prostate
CC neoplastic condition. The present sequence encodes human XIAP.
XX
SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
Query Match 100.0%; Score 198; DB 12; Length 2540;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCGCTT 60
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAAGCCCTTGGGACCAACATGCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGTGAAGCCCTTGGGACCAACATGCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTAGTGAAGCCCTTGGGACCAACATGCTTTCACTGTGGA 180
DB 946 GGAGGGCTAACTGATTTAGTGAAGCCCTTGGGACCAACATGCTTTCACTGTGGA 1005
QY 181 CCAGGGTCAAAATATCTG 198
DB 1006 CCAGGGTCAAAATATCTG 1023
Search completed: October 22, 2004, 20:24:53
Job time : 264 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 20:15:23 ; Search time 54 Seconds
(without alignments)
2606.226 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaagcacggatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1645014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B-COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A-COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B-COMB.seq:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	198	100.0	1588	3	US-09-239-867-3	Sequence 3, Appli
2	198	100.0	1588	4	US-10-024-433-3	Sequence 3, Appli
3	198	100.0	1659	4	US-09-016-434-1053	Sequence 1053, Ap
4	198	100.0	2540	2	US-08-511-485-3	Sequence 3, Appli
5	198	100.0	2540	3	US-09-392-580-1	Sequence 1, Appli
6	198	100.0	2540	4	US-09-201-936-3	Sequence 3, Appli
7	198	100.0	2540	4	US-09-023-655-900	Sequence 900, App
8	198	100.0	2540	4	US-09-011-356-3	Sequence 3, Appli
9	198	100.0	2540	4	US-09-672-717-218	Sequence 218, App
10	198	100.0	2540	4	US-09-201-932-3	Sequence 3, Appli
11	198	100.0	3000	4	US-09-672-717-231	Sequence 231, App
12	198	100.0	5232	3	US-09-212-971-3	Sequence 3, Appli
13	198	100.0	5232	3	US-08-800-929A-3	Sequence 3, Appli
14	198	100.0	5232	3	US-09-617-053A-3	Sequence 3, Appli
15	173	87.4	2100	2	US-08-511-485-9	Sequence 9, Appli
16	173	87.4	2100	4	US-09-201-936-9	Sequence 9, Appli
17	173	87.4	2100	4	US-09-011-356-9	Sequence 9, Appli
18	173	87.4	2100	4	US-09-672-717-224	Sequence 224, App
19	173	87.4	2100	4	US-09-201-932-9	Sequence 9, Appli
20	169.8	85.8	2691	3	US-09-212-971-9	Sequence 9, Appli
21	169.8	85.8	2691	3	US-08-800-929A-9	Sequence 9, Appli
22	169.8	85.8	2691	3	US-09-617-053A-9	Sequence 9, Appli
23	164.4	83.0	711	3	US-09-121-979-3	Sequence 3, Appli
24	164.4	83.0	711	3	US-09-332-319-3	Sequence 3, Appli
25	164.4	83.0	1559	3	US-09-239-867-1	Sequence 1, Appli
26	164.4	83.0	1559	4	US-10-024-433-1	Sequence 1, Appli
27	157.8	79.7	152331	3	US-09-128-155-16	Sequence 16, Appli

c

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28 131.4 66.4 176373 3 US-09-128-155-17 Sequence 17, Appli
29 78.6 39.7 1448 4 US-09-579-692B-57 Sequence 57, Appli
30 78.6 39.7 2563 4 US-09-016-434-1076 Sequence 1076, Ap
31 78.6 39.7 2563 4 US-09-023-655-894 Sequence 894, App
32 78.6 39.7 2601 3 PCT-US96-12860-3 Sequence 3, Appli
33 78.6 39.7 2601 5 US-08-511-485-5 Sequence 3, Appli
34 78.6 39.7 2676 2 US-08-511-485-5 Sequence 5, Appli
35 78.6 39.7 2676 4 US-09-201-936-5 Sequence 220, App
36 78.6 39.7 2676 4 US-09-011-356-5 Sequence 5, Appli
37 78.6 39.7 2676 4 US-09-672-717-220 Sequence 5, Appli
38 78.6 39.7 2676 4 US-09-201-932-5 Sequence 5, Appli
39 78.6 39.7 2916 4 US-09-814-915A-31 Sequence 31, Appli
40 78.6 39.7 3076 2 US-09-205-144-1 Sequence 1, Appli
41 78.6 39.7 3076 4 US-09-814-915A-11 Sequence 11, Appli
42 78.6 39.7 3734 4 US-09-579-692B-7 Sequence 7, Appli
43 78.6 39.7 6669 3 US-09-212-971-5 Sequence 5, Appli
44 78.6 39.7 6669 3 US-08-800-929A-5 Sequence 5, Appli
45 78.6 39.7 6669 3 US-09-617-053A-5 Sequence 5, Appli

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ALIGNMENTS

RESULT 1

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US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

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Query Match 100.0%; Score 198; DB 3; Length 1588;
Best Local Similarity 100.0%; Pred. No. 1.9e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TATGAAGCAGCGATCTTTTACCTTTGGGACATGGATATACCTAGTTTAAAGAGAGAGCTT 60
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Db 826 TATGAAGCAGCGATCTTTTACCTTTGGGACATGGATATACCTAGTTTAAAGAGAGAGCTT 885
      |||||

Qy 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGAAGTAAAGTCTTTTCACTGTGGA 120
      |||||
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGAAGTAAAGTCTTTTCACTGTGGA 945
      |||||

Qy 121 GGAGGGCTAACTGATTTGAAGCCCAAGAGACCTTTGGGAACCAACATGCTAAATGGTAT 180
      |||||
Db 946 GGAGGGCTAACTGATTTGAAGCCCAAGAGACCTTTGGGAACCAACATGCTAAATGGTAT 1005
      |||||

Qy 181 CCAGGGTGCATATCTG 198
      |||||
Db 1006 CCAGGGTGCATATCTG 1023
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RESULT 2

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US-10-024-433-3
; Sequence 3, Application US/10024433
; Patent No. 6797473
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: MALE FERTILITY

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; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-024-433-3

Query Match 100.0%; Score 198; DB 4; Length 1588;
Best Local Similarity 100.0%; Pred. No. 1.9e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 180
Db 946 GGAGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 3
US-09-616-434-1053
; Sequence 1053, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREWITH
; APPLICATION NUMBER: US/09/016,434
; PRIOR APPLICATION DATA:
; CLASSIFICATION:
; FILING DATE:
; APPLICATION NUMBER:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1053:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1016687
US-09-016-434-1053

Query Match 100.0%; Score 198; DB 4; Length 1659;
Best Local Similarity 100.0%; Pred. No. 1.9e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 60
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QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 934 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 993

QY 121 GGAGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 180
Db 994 GGAGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 1053

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 4
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 100.0%; Score 198; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTTGGAAGCCCTGAGACCCCTGGGAACCAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTTGGAAGCCCTGAGACCCCTGGGAACCAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAATATCTG 198
DB 1006 CCAGGGTGCAATATCTG 1023

RESULT 5

US-09-392-580-1
; Sequence 1, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)
US-09-392-580-1

Query Match 100.0%; Score 198; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 885

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DB 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTTGGAAGCCCTGAGACCCCTGGGAACCAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTTGGAAGCCCTGAGACCCCTGGGAACCAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAATATCTG 198
DB 1006 CCAGGGTGCAATATCTG 1023

RESULT 6

US-09-201-936-3
; Sequence 3, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)..(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTTGGAAGCCCTGAGACCCCTGGGAACCAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTTGGAAGCCCTGAGACCCCTGGGAACCAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAATATCTG 198
DB 1006 CCAGGGTGCAATATCTG 1023

RESULT 7

US-09-023-655-900
; Sequence 900, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMEUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH

2/9/98


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US-09-201-932-3
; Sequence 3, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-932-3

Query Match      100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 11
US-09-672-717-231
; Sequence 231, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 3000

US-09-201-932-3
; TYPE: DNA
; ORGANISM: Homo sapiens
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-932-3

Query Match      100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 12
US-09-212-971-3
; Sequence 3, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4623)...(4623)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4622)...(4622)
; OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3

Query Match      100.0%; Score 198; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 3.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGGA 120
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Db      886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCAGTGTGA 945
QY      121 GGAGGCTAACTGATGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db      946 GGAGGCTAACTGATGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY      181 CCAGGCTGCAAAATATCTG 198
Db      1006 CCAGGCTGCAAAATATCTG 1023

RESULT 13
US-08-800-929A-3
; Sequence 3, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...5232
; OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.
US-08-800-929A-3

Query Match 100.0%; Score 198; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 3.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGACGAGCTT 60
Db      826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGACGAGCTT 885
QY      61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCAGTGTGA 120
Db      886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCAGTGTGA 945
QY      121 GGAGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db      946 GGAGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY      181 CCAGGCTGCAAAATATCTG 198
Db      1006 CCAGGCTGCAAAATATCTG 1023

RESULT 14
US-09-617-053A-3
; Sequence 3, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4623)...(4623)
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: (4622)...(4622)
; OTHER INFORMATION: n can be any nucleotide
US-09-617-053A-3

Query Match 100.0%; Score 198; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 3.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15

US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 87.4%; Score 173; DB 2; Length 2100;
Best Local Similarity 92.4%; Pred.No.1.2e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db |||||
Qy 916 TATGAGCAGCGATCTTTACTTTTGGACATGGATATCTCAGTTAACAGGAGCAGCTT 975
Db |||||
Qy 61 GCAAGAGCTGGATTATGCTTTAGTGAAGTGATAAAGTGAAGTCTTCACTGTGGA 120
Db |||||
Qy 976 GCAAGAGCTGGATTATGCTTTAGTGAAGTGATAAAGTGAAGTCTTCACTGTGGA 1035
Db |||||
Qy 121 GGAGGCTAACTGATTGGAGCCAGTGAAGCCCTTGGGACACATGCTAAATGGTAT 180
Db |||||
Qy 1036 GGAGGCTCAGGATTGGAGCCAGTGAAGCCCTTGGGACACATGCTAAATGGTAT 180
Db |||||
Qy 181 CCAGGGTGCAATATCT 197
Db |||||
Qy 1096 CCAGGGTGCAATATCT 1112
Db |||||

Search completed: October 22, 2004, 22:14:05
Job time : 55 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 20:10:53 ; Search time 1727.5 Seconds
(without alignments)
4176.594 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaagacaggtatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query §		DB	ID	Description	
		Match	Length				
1	180.4	91.1	533	7	CN315131	170004179	
2	166	83.8	1851	3	BC056914	Homo sapi	
3	164.6	83.1	773	6	CD350778	UI-M-G10-	
4	164.4	83.0	1789	3	BC046168	Homo sapi	
c	157.4	79.5	628	1	AI573382	mm83e12.x	
6	114	57.6	1177	4	BM805359	AGENCOURT	
7	112	56.6	536	1	AU123207	AU123207	
8	104.4	52.7	716	1	AV706807	AV706807	
c	100.2	50.6	318	2	BF659610	BF659610	
10	99	50.0	617	2	BF663325	uz88e12.x	
c	11	96.4	48.7	721	9	CE100865	BF663325
12	94.4	47.7	504	2	BB650856	tigr-gss-	
c	13	91.6	46.3	334	4	BM220130	BB650856
c	14	91.6	46.3	334	5	BQ552032	BM220130
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c	16	87	43.9	420	8	AQ011995	H4013A06-
17	85	42.9	1494	9	AY398943	CF222542	
18	84	42.4	849	8	BZ242580	AGENCOURT	
19	80.6	40.7	373	6	BU662508	HS_2190_A	
20	79.4	40.1	663	5	BU658508	AY398943	
21	78.6	39.7	354	2	AW375598	Homo sapi	
22	78.6	39.7	354	2	AW375599	CH230-252	
23	78.6	39.7	402	2	AW846507	BU662508	
24	78.6	39.7	531	2	AW375599	BY662508	
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25	78.6	39.7	532	2	AW846425	QV0-CT017
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27	78.6	39.7	571	2	AW375649	QV0-CT017
28	78.6	39.7	582	2	AW846337	QV0-CT017
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30	78.6	39.7	621	2	AW375648	QV0-CT017
31	78.6	39.7	680	2	AW375625	QV0-CT017
32	78.6	39.7	886	5	BQ652590	AGENCOURT
33	78.6	39.7	1472	9	AY398945	Mus muscu
34	78.6	39.7	1799	9	AY420753	Homo sapi
35	78.4	39.6	269	2	BE506790	db87g08.y
36	77	38.9	997	7	C0646846	ILLUMIGEN
37	77	38.9	1045	7	CN645252	ILLUMIGEN
38	76.6	38.7	887	4	BJ728878	BJ728878
39	75.6	38.2	498	1	AJ678724	AJ678724
40	74.4	37.6	441	4	BM312708	ig78a10.y
41	74.4	37.6	563	1	AA702174	z191g08.s
42	74.4	37.6	652	1	AV704923	AV704923
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ALIGNMENTS

RESULT 1
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LOCUS CN315131 533 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000417981828 GRN_Es Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN315131
VERSION CN315131.1 GI:47331545
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 533)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 533 Std Error: 0.00.

FEATURES

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1..533
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone.lib="GRN ES"
/note="oligo dt-primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 91.1%; Score 180.4; DB 7; Length 533;
Best Local Similarity 94.4%; Pred. No. 2.3e-45;
Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 1 TATGAAGCAGGATCTTTACTTTTGGGACATGATATCTACTAGTTTAAAGAGCAGCTT 60
Db 155 TATGAAGCAGGATCTTTACTTTTGGGATGGATATATTCAGTTTAAAGAGCAGCTT 214

QY 61 GCAAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
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 Db 215 TCAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 274
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 QY 121 GGAGGCTAACTGATTGGAGCCAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
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 QY 181 CCAGGCTGCAAAATATCTG 198
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 Db 335 CCAGGCTGAAATATCTG 352
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 BC056914
 LOCUS
 DEFINITION
 Homo sapiens baculoviral IAP repeat-containing 8, mRNA (cDNA clone IMAGE:5742924), with apparent retained intron.
 ACCESSION
 BC056914
 VERSION
 BC056914.1 GI:34784469
 KEYWORDS
 HTC.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1851)
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zerbber B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raja S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Rodrigues S., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1851)
 Strausberg R.
 Direct Submission
 Submitted (25-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
 DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: <http://image.llnl.gov>
 Series: IRAC Plate: 119 Row: h Column: 2
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16974127
 This clone has the following problem: retained intron.

FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742924"
 /tissue_type="Brain, adult medulla"
 /clone_lib="NIH MGC_119"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN
 Query Match 83.8%; Score 166; DB 3; Length 1851;
 Best Local Similarity 89.9%; Pred. No. 1.1e-40;
 Matches 178; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGATATCTCACTTAAAGGAGCAGCTT 60
 Db 1062 TATGAAGCCCGGCTCATTTACTTTTGGACATGATGTACTCCGTTAAACAAGACGAGCTT 1121
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 QY 61 GCAAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
 |||||
 Db 1122 GCAAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 1181
 |||||
 QY 121 GGAGGCTAACTGATTGGAGCCAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
 |||||
 Db 1182 GGAGGCTAGCCAACTGGAGCCAGGAGAGATCTTGGACAGCATGCTAAATGGTAT 1241
 |||||
 QY 181 CCAGGCTGCAAAATATCTG 198
 |||||
 Db 1242 CCAGGCTGCAAAATATCTG 1259
 |||||

RESULT 3
 CD350778 773 bp mRNA linear EST 09-JUL-2003
 UI-M-GIO-cgh-g-23-0-UI.r1 NIH BMAP_GIO Mus musculus cDNA clone
 IMAGE:6853392 5', mRNA sequence.
 CD350778
 CD350778.1 GI:31142365
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 773)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1..773
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6853392"

FEATURES
 source

/tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP G10"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCGAGACAG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 83.1%; Score 164.6; DB 6; Length 773;
 Best Local Similarity 92.5%; Pred. No. 2.2e-40;
 Matches 173; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 11 GGATCTTTACTTTTGGGACATGATATCTAGTTAAACAAGGAGCGAGCTTGCAAGAGCTG 70
 Db 1 GGATCTTTACTTTTGGGACATGATATCTAGTTAAACAAGGAGCGAGCTTGCAAGAGCTG 60

QY 71 GATTTTATCTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGAGGAGGCTAA 130
 Db 61 GATTTTATCTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGAGGAGGCTCA 120

QY 131 CTGATTGGAAGCCCGAGTGAAGCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCA 190
 Db 121 CGGATTGGAAGCCCGAGTGAAGCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCA 180

QY 191 AATACT 197
 Db 181 AATACT 187

RESULT 4

BC046168
 LOCUS
 DEFINITION Homo sapiens, similar to baculoviral IAP repeat-containing 8, clone IMAGE:5742590, mRNA.

ACCESSION BC046168
 VERSION BC046168.1 GI:28374455
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1789)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (31-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapsb-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) md@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 107 Row: 1 Column: 1
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
 This clone has the following problem: frame shifted.

FEATURES source

Location/Qualifiers
 1..1789
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742590"
 /tissue_type="Brain, adult medulla"
 /clone_lib="NIH MGC_119"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 83.0%; Score 164.4; DB 3; Length 1789;
 Best Local Similarity 89.4%; Pred. No. 3.4e-40;
 Matches 177; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGATATCTAGTTAAACAAGGAGCGAGCTT 60
 Db 1002 TATGAAGCCCGCTCAATTTTGGGACATGATGTTCTCGTCAACAAGGAGCGAGCTT 1061

QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGGAAGGTGATAAAGTAAAGTGTCTTCACTGTGGA 120
 Db 1062 GCAAGAGCTGGATTTTATGCTTAGTCAAGAGGATAAAGTACAGTGTCTTCACTGTGGA 1121

QY 121 GGAGGCTTAAGTATGGAAGCCCGAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
 Db 1122 GGAGGCTTAGCCCACTGGAAGCCCAAGGAAGATCTTGGGAACAGCATGCTAAATGGTAT 1181

QY 181 CCAGGCTGCAAAATATCTG 198
 Db 1182 CCAGGTTGCAAAATATCTG 1199

RESULT 5

AI573382/c
 LOCUS
 DEFINITION mm83e12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. ;, mRNA sequence.

ACCESSION AI573382
 VERSION AI573382.1 GI:4536756
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 628)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,I., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 440.

FEATURES source

Location/Qualifiers
 1..628

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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse Tcell 937311"
/notes="Organ: blood; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dr. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTGTGTTTTTTTTT 3'"

ORIGIN
Query Match 79.5%; Score 157.4; DB 1; Length 628;
Best Local Similarity 90.4%; Pred. No. 3.9e-38;
Matches 178; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 1 TATGAAGCAGGATCTTTTACTTTTGGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
|
|
|
Db 604 TATGAAGCAGGATCGTTACTTTTGGNACATGACATCCTCAGTTACAAAGGAGCAGCTT 545
|
|
|
QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGGAAGGTGATAAAGTCTTTCTACTGTGGA 120
|
|
|
Db 544 GCAAGAGCT-GAATTTATGCTTTTAGTTGAAGGCGATAAAGTGAAGTCTTTCTACTGTGGA 486
|
|
|
QY 121 GGAGGGCTACTGATGGAGCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|
|
|
Db 485 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTTGGGAACAGCATGCGAAGTGGTAC 426
|
|
|
QY 181 CCAGGGTGCAATATCT 197
|
|
|
Db 425 NCAGGGTGCAATATCT 409
|
|
|

RESULT 6
BM805359
LOCUS
DEFINITION 1177 bp mRNA linear EST 05-MAR-2002
AGENCOURT 6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
5', mRNA sequence.
ACCESSION BM805359
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota.T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K.,
Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y.,
Ishii,S., Saito,K., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
source
1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM1000921"
/cell_type="teratocarcinoma"
/line="NT2"
/clone_lib="NT2RM1"
/notes="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN
Query Match 56.6%; Score 112; DB 1; Length 536;
Best Local Similarity 98.2%; Pred. No. 5.9e-24;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 85 GGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGAGGAGGCTTAAGTGAAGCC 144
|
|
|
Db 99 GGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGAGGAGGCTTAAGTGAAGCC 158
|
|
|
QY 145 AGTGAAGCCCTTGGGAACAACATGCTAAATGCTATCCAGGGTGCAATATCTG 198
|
|
|

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(destroyed); Site 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dr primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN
Query Match 57.6%; Score 114; DB 4; Length 1177;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGAGGAGGCTTAAGTGAAGCC 144
|
|
|
Db 142 GGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGAGGAGGCTTAAGTGAAGCC 201
|
|
|
QY 145 AGTGAAGCCCTTGGGAACAACATGCTAAATGCTATCCAGGGTGCAATATCTG 198
|
|
|
Db 202 AGTGAAGCCCTTGGGAACAACATGCTAAATGCTATCCAGGGTGCAATATCTG 255
|
|
|

RESULT 7
AUI23207
LOCUS
DEFINITION 536 bp mRNA linear EST 01-AUG-2002
AUI23207 NT2RM1 Homo sapiens cDNA clone NT2RM1000921 5', mRNA
sequence.
ACCESSION AUI23207
VERSION AUI23207.1 GI:10947923
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota.T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K.,
Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y.,
Ishii,S., Saito,K., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
source
1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM1000921"
/cell_type="teratocarcinoma"
/line="NT2"
/clone_lib="NT2RM1"
/notes="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN
Query Match 56.6%; Score 112; DB 1; Length 536;
Best Local Similarity 98.2%; Pred. No. 5.9e-24;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 85 GGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGAGGAGGCTTAAGTGAAGCC 144
|
|
|
Db 99 GGTGAAGGTGATAAAGTAAAGTGCCTTCACTGTGAGGAGGCTTAAGTGAAGCC 158
|
|
|
QY 145 AGTGAAGCCCTTGGGAACAACATGCTAAATGCTATCCAGGGTGCAATATCTG 198
|
|
|

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Db 159 AGTGAACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATATCTG 212

RESULT 8
 AV706807 716 bp mRNA linear EST 09-OCT-2000
 LOCUS AV706807 ADB Homo sapiens cDNA clone ADBCOF01 5', mRNA sequence.
 DEFINITION AV706807
 ACCESSION AV706807
 VERSION AV706807.1 GI:10724085
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 716)
 AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,
 Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,
 Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,
 Zhong, M., Lu, G., Hu, R., Chen, J., Chen, J., Chen, Z. and Han, Z.
 TITLE Homo sapiens cDNA ADB clones
 JOURNAL Unpublished (2000)
 COMMENT Contact: Zequang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 FEATURES
 source Location/Qualifiers
 1..716
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ADBCOF01"
 /tissue_type="Adrenal gland"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="ADB"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"
 ORIGIN
 Query Match 52.7%; Score 104.4; DB 1; Length 716;
 Best Local Similarity 94.7%; Pred. No. 1.5e-21;
 Matches 108; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 85 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGAGGGCTAACTGATGGAAGCCC 144
 Db 156 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGAGGGCTAACTGATGGAAGCCC 215
 QY 145 AGTCAGACCCCTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATATCTG 198
 Db 216 AGTGAACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGAAGAACTACTG 269

RESULT 9
 BF659610/c 318 bp mRNA linear EST 29-DEC-2000
 LOCUS BF659610 u28he12.x1 NCI_CGAP Lu29 Mus musculus cDNA clone IMAGE:3676174 3',
 DEFINITION similar to SW:1AP3_MOUSE Q60989 INHIBITOR OF APOPTOSIS PROTEIN 3 ; ,
 EST. mRNA sequence.
 ACCESSION BF659610
 VERSION BF659610.1 GI:11924744
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 318)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 image.lnl.gov/image/html/iresources.shtml

MGI:1436942
 Possible reversed clone: polyT not found
 Seq primer: -40UP from Gibco
 High quality sequence stop: 226.
 Location/Qualifiers
 1. .318
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH II"
 /db_xref="taxon:10090"
 /clone="IMAGE:3676174"
 /tissue_type="spontaneous tumor, metastatic to mammary.
 Stem cell origin."
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu29"
 /notes="lung; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN
 Query Match 50.6%; Score 100.2; DB 2; Length 318;
 Best Local Similarity 92.9%; Pred. No. 2.5e-20;
 Matches 105; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 53 AGCAGCTTGCACAGCTGGATTTATGCTTTAGTGAAGTGATAAAGTAAAGTCTTTC 112
 |||||
 Db 317 AGCAGCTTGCACAGCTGGATTTATGCTTTAGTGAAGTGATAAAGTCAAGTCTTTC 258
 |||||

QY 113 ACTGTGGAGGAGGGCTAACTGATGTGAGCCCACTGAGACCCCTTGGGACAA 165
 |||||
 Db 257 ACTGTGGAGGAGGGCTCTCGATTTGGAAGCAAGTGAAGACCCCTTGGGACAA 205
 |||||

RESULT 10
 BB663325 617 bp mRNA linear EST 26-OCT-2001
 LOCUS
 DEFINITION BB663325 RIKEN full-length enriched, 15 days embryo head Mus
 musculus cDNA clone D930039G22 5', mRNA sequence.
 ACCESSION BB663325
 VERSION BB663325.1 GI:16497079
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 617)
 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,O.,
 Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sugabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
 Takeda,Y., Tanaka,T., Toyota,I., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 UNPUBLISHED (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

TITLE
 JOURNAL
 COMMENT

by Yulan Piao (NIA)."

ORIGIN

Query Match 46.3%; Score 91.6; DB 4; Length 334;
 Best Local Similarity 91.5%; Pred. No. 1.2e-17;
 Matches 97; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 82 TTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAACTGATTGGAAG 141
 |||||
 Db 260 TTAGGTGAAGGCGATAAAGTCAAGTGTCTTTCACGTGTGGAGGAGGCTCAGGATTGGAAG 201
 |||||

QY 142 CCACGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGT 187
 |||||
 Db 200 CCAAGTGAAGACCCCTTGGGAACAACATGCTAAAGTGGTACCAGGGT 155
 |||||

RESULT 14

BO552032/c
 LOCUS
 DEFINITION H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
 H4013A06 3', mRNA sequence.

ACCESSION BO552032

VERSION BO552032.1 GI:21452918

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,

Martin, P.R., Staggs, C.A., Basse, J., Aiba, K., Hamatani, T.,

Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H.

Assembly, verification, and initial annotation of NIA 7.4K mouse

cDNA clone set

Genome Res. 12 (12), 1999-2003 (2002)

JOURNAL 22354164

MEDLINE 12466305

PUBMED

COMMENT Other ESTs: H4013A06-5

Contact: Yong Qian

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA

Email: cdna@nslgscn.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please

visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.

Plate: H4013 row: A column: 06

Seq primer: -21M13 Forward

High quality sequence stop: 584

POLYA=Yes.

FEATURES

source

1..584
 /location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="niaEST:H4013A06-3"
 /db_xref="taxon:10090"
 /clone="H4013A06"
 /sex="mixed"
 /dev_stage="mixed"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."

ORIGIN

Query Match 46.3%; Score 91.6; DB 5; Length 584;
 Best Local Similarity 91.5%; Pred. No. 1.5e-17;
 Matches 97; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 82 TTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAACTGATTGGAAG 141
 |||||
 Db 260 TTAGGTGAAGGCGATAAAGTCAAGTGTCTTTCACGTGTGGAGGAGGCTCAGGATTGGAAG 201
 |||||

QY

142 CCACGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGT 187
 |||||
 Db 200 CCAAGTGAAGACCCCTTGGGAACAACATGCTAAAGTGGTACCAGGGT 155
 |||||

RESULT 15

CF222542

LOCUS

DEFINITION

AGENCOURT_14926978 NICHG XGC Emb5 mRNA linear EST 04-AUG-2003

IMAGE:6981334 5', mRNA sequence.

ACCESSION CF222542

VERSION CF222542.1 GI:33423250

KEYWORDS EST.

SOURCE

ORGANISM

Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 791)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs@email.nih.gov

Tissue Procurement: Robert M. Grainger

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM14642 row: f column: 21

High quality sequence start: 3

High quality sequence stop: 735.

Location/Qualifiers

1..791

/organism="Xenopus tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="IMAGE:6981334"

/tissue_type="gastrula"

/dev_stage="embryo, stages 10-13"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NICHG XGC Emb5"

/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;

Cloned unidirectionally. Primer: Oligo dt. Average insert

size 2.0 Kb. Constructed by Invitrogen. Note: This is a

Xenopus Gene Collection (XGC) library."

ORIGIN

Query Match

Best Local Similarity 45.9%; Score 90.8; DB 6; Length 791;

Matches 131; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 1 TATGAAGCACCGATCTTTTACTTTTGGGACATGATATACTAGTTAAACAGGACGCTT 60

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Db 267 TACATGCTCGTCTTGAGACCTTTTCATCATGGTCTATTCCAAATTGACAGGAACATCTC 326

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QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACGTGGA 120

|||

Db 327 GCTAAAGCTGGATTCTATAGTATAGGTGACGAGATGCCAAAGTGTCTTTCATTGTGG 386

|||

QY 121 GGAGGCTTAACTGATTGGAAGCCCAAGTCAAGACCTTCGGACAACATGCTAAATGGTAT 180

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Db 387 GGAGTGTAAATGTTGTGCGCAACATGATCTTTGGGAAGCATGCCAAGGCATAT 446

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QY 181 CCAGGCTCAAAATATCTG 198

|||

Db 447 CTGTGATCAAGTTCTCTG 464

Search completed: October 22, 2004, 22:12:14
Job time : 1732.5 secs

EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 2100
TYPE: DNA
ORGANISM: Mus musculus
US-09-201-936-9

Query Match 87.4%; Score 173; DB 9; Length 2100;
Best Local Similarity 92.4%; Pred. No. 2.9e-46;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGACGCTT 60
DB 916 TATGAAGCAGCGATCGTTTACTTTTGGAAATGGATATCTCAGTTAAACAGGACGCTT 975
QY 61 GCAAGAGCTGGATTTATGCTTTAGCTGAAGTGATAAGTAAAGTCTTTCACCTGTGGA 120
DB 976 GCAAGAGCTGGATTTATGCTTTAGCTGAAGCGGATAAGTAAAGTCTTTCACCTGTGGA 1035
QY 121 GGAGGCTTAACGTGTTGAAGCCAGTGAAGACCCCTTGGGAACAAATGCTTAATGGTAT 180
DB 1036 GGAGGCTTACGGATGGAGCCAAAGTGAAGACCCCTTGGACCATGCTTAAGTGCTAC 1095
QY 181 CCAGGCTGCAATATCT 197
DB 1096 CCAGGCTGCAATATCT 1112

RESULT 14
US-10-636-065-224
Sequence 224, Application US/10636065
Publication No. US20040127694A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: LaCasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 224
LENGTH: 2100
TYPE: DNA
ORGANISM: Mus musculus
US-10-636-065-224
Query Match 87.4%; Score 173; DB 17; Length 2100;
Best Local Similarity 92.4%; Pred. No. 2.9e-46;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGACGCTT 60
DB 916 TATGAAGCAGCGATCGTTTACTTTTGGAAATGGATATCTCAGTTAAACAGGACGCTT 975
QY 61 GCAAGAGCTGGATTTATGCTTTAGCTGAAGTGATAAGTAAAGTCTTTCACCTGTGGA 120
DB 976 GCAAGAGCTGGATTTATGCTTTAGCTGAAGCGGATAAGTAAAGTCTTTCACCTGTGGA 1035
QY 121 GGAGGCTTAACGTGTTGAAGCCAGTGAAGACCCCTTGGGAACAAATGCTTAATGGTAT 180

DB 1036 GGAGGCTCAGGATTTGAAGCCAACTGAAGACCCCTTGGACCAAGCAT
QY 181 CCAGGCTGCAATATCT 197
DB 1096 CCAGGCTGCAATATCT 1112

RESULT 15
US-10-600-272-9
Sequence 9, Application US/10600272
Publication No. US20040157232A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003006
CURRENT APPLICATION NUMBER: US/10/600,272
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/011,356
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: PCT/IB96/01022
PRIOR FILING DATE: 1996-08-05
PRIOR APPLICATION NUMBER: US 08/576,956
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: US 08/511,485
PRIOR FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2100
TYPE: DNA
ORGANISM: Mus musculus
US-10-600-272-9

Query Match 87.4%; Score 173; DB 17; Length 2100;
Best Local Similarity 92.4%; Pred. No. 2.9e-46;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGACGCTT 60
DB 916 TATGAAGCAGCGATCGTTTACTTTTGGAAATGGATATCTCAGTTAAACAGGACGCTT 975
QY 61 GCAAGAGCTGGATTTATGCTTTAGCTGAAGTGATAAGTAAAGTCTTTCACCTGTGGA 120
DB 976 GCAAGAGCTGGATTTATGCTTTAGCTGAAGCGGATAAGTAAAGTCTTTCACCTGTGGA 1035
QY 121 GGAGGCTTAACGTGTTGAAGCCAGTGAAGACCCCTTGGGAACAAATGCTTAATGGTAT 180
DB 1036 GGAGGCTTACGGATGGAGCCAAAGTGAAGACCCCTTGGACCATGCTTAAGTGCTAC 1095
QY 181 CCAGGCTGCAATATCT 197
DB 1096 CCAGGCTGCAATATCT 1112

Search completed: October 22, 2004, 23:34:23
Job time : 243 secs

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; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)....(2540)
; OTHER INFORMATION: N may be any nucleotide
US-10-600-272-3

Query Match      100.0%; Score 198; DB 17; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTT 60
Db      826  TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTT 885

QY      61  GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db      886  GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY      121  GGAGGCTAACTGATTGGAGCCAGTGAAGCCCTTGGACAAACATGCTAAATGGTAT 180
Db      946  GGAGGCTAACTGATTGGAGCCAGTGAAGCCCTTGGACAAACATGCTAAATGGTAT 1005

QY      181  CCAGGCTGCAATATCTG 198
Db      1006  CCAGGCTGCAATATCTG 1023

RESULT 11
US-10-636-065-231
; Sequence 231, Application US/10636065
; Publication No. US200401276941
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-636-065-231

Query Match      100.0%; Score 198; DB 17; Length 3000;
Best Local Similarity 100.0%; Pred. No. 2e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTT 60
Db      1482  TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTT 1541

QY      61  GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db      1542  GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 1601

QY      121  GGAGGCTAACTGATTGGAGCCAGTGAAGCCCTTGGACAAACATGCTAAATGGTAT 180
Db      1602  GGAGGCTAACTGATTGGAGCCAGTGAAGCCCTTGGACAAACATGCTAAATGGTAT 1661

QY      181  CCAGGCTGCAATATCTG 198
Db      1662  CCAGGCTGCAATATCTG 1679

RESULT 12
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NACP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

Query Match      100.0%; Score 198; DB 9; Length 5232,
Best Local Similarity 100.0%; Pred. No. 2.5e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTT 60
Db      826  TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTT 885

QY      61  GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db      886  GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY      121  GGAGGCTAACTGATTGGAGCCAGTGAAGCCCTTGGACAAACATGCTAAATGGTAT 180
Db      946  GGAGGCTAACTGATTGGAGCCAGTGAAGCCCTTGGACAAACATGCTAAATGGTAT 1005

QY      181  CCAGGCTGCAATATCTG 198
Db      1006  CCAGGCTGCAATATCTG 1023

RESULT 13
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
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Sat Oct 23 17:44:28 2004

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; Sequence 900, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 900:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1184319
; SEQUENCE DESCRIPTION: SEQ ID NO: 900 :
US-10-641-643-900

Query Match 100.0%; Score 198; DB 16; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAACGACGGATCTTTACTTTTGGACATGGATATCTAGTAAAGTAAAGTCTTCACTGTGGA 60
DB 826 TATGAACGACGGATCTTTACTTTTGGACATGGATATCTAGTAAAGTAAAGTCTTCACTGTGGA 885
QY 61 GCAGAGCTGATTTTATGCTTTAGTGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAGAGCTGATTTTATGCTTTAGTGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 180
DB 946 GGAGGGCTAACTGATTTGGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 1005

RESULT 9
US-10-636-065-218
; Sequence 218, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2540)
; OTHER INFORMATION: n=a,t,c, or g
; US-10-636-065-218

Query Match 100.0%; Score 198; DB 17; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAACGACGGATCTTTACTTTTGGACATGGATATCTAGTAAAGTAAAGTCTTCACTGTGGA 60
DB 826 TATGAACGACGGATCTTTACTTTTGGACATGGATATCTAGTAAAGTAAAGTCTTCACTGTGGA 885
QY 61 GCAGAGCTGATTTTATGCTTTAGTGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAGAGCTGATTTTATGCTTTAGTGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 180
DB 946 GGAGGGCTAACTGATTTGGAAGCTGATTAAGTAAAGTCTTCACTGTGGA 1005

RESULT 10
US-10-600-272-3
; Sequence 3, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander B.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens

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Db 1006 CCAGGGTGCAAAATATCTG 1023
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RESULT 5
US-10-007-926A-274
; Sequence 274, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUGAITE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 274
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: baculoviral iap repeat-containing 4 (BIRC4)
US-10-007-926A-274

Query Match 100.0%; Score 198; DB 15; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCTGATAAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCTGATAAAGTAAAGTCTTTCACTGTGGA 945

Qy 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTTAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTTAATGGTAT 1005

Qy 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 6
US-10-366-307-1
; Sequence 1, Application US/10366307
; Publication No. US20030224399A1
; GENERAL INFORMATION:
; APPLICANT: Read, John C.
; TITLE OF INVENTION: Methods for Determining the Prognosis
; FILE REFERENCE: P-LJ 5659
; CURRENT APPLICATION NUMBER: US/10/366,307
; CURRENT FILING DATE: 2003-02-12
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 198; DB 15; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCTGATAAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCTGATAAAGTAAAGTCTTTCACTGTGGA 945

Qy 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTTAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTTAATGGTAT 1005

Qy 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 7
US-10-388-360-331
; Sequence 331, Application US/10388360
; Publication No. US2003022528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-331

Query Match 100.0%; Score 198; DB 15; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCTGATAAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCTGATAAAGTAAAGTCTTTCACTGTGGA 945

Qy 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTTAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTTAATGGTAT 1005

Qy 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 8
US-10-641-643-900
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Sat Oct 23 17:44:28 2004

Db 946 GGAGGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

Qy 181 CCAGGGTGCAAAATATCTG 198
 Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 2
 US-10-305-720-1053
 ; Sequence 1053, Application US/10305720
 ; Publication No. US20040010136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
 ; FILE REFERENCE: PA-0002-1 CON
 ; CURRENT APPLICATION NUMBER: US/10/305,720
 ; PRIOR FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: 09/016,434
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 1490
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1053
 ; LENGTH: 1659
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: GenBank ID No. US20040010136A1 gi1016687
 US-10-305-720-1053

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 Best Local Similarity 100.0%; Pred. No. 1.5e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TATGAAGCAGGATCTTTTCTTTGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 60
 Db 874 TATGAAGCAGGATCTTTTCTTTGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 933
 Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
 Db 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 993
 Qy 121 GGAGGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 Db 994 GGAGGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053
 Qy 181 CCAGGGTGCAAAATATCTG 198
 Db 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 3
 US-09-964-899-38
 ; Sequence 38, Application US/09964899
 ; Patent No. US20020174446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Dalia et al.
 ; TITLE OF INVENTION: Identification of Genes Involved in
 ; FILE REFERENCE: 4-31612 A
 ; CURRENT APPLICATION NUMBER: US/09/964,899
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,893
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/298,309
 ; PRIOR FILING DATE: 2001-06-14
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 2404
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-964-899-38

Query Match 100.0%; Score 198; DB 9; Length 2404;
 Best Local Similarity 100.0%; Pred. No. 1.8e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 827 TATGAAGCAGGATCTTTTCTTTGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 886
 Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
 Db 987 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 946
 Qy 121 GGAGGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 Db 947 GGAGGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1006
 Qy 181 CCAGGGTGCAAAATATCTG 198
 Db 1007 CCAGGGTGCAAAATATCTG 1024

RESULT 4
 US-09-201-936-3
 ; Sequence 3, Application US/09201936
 ; Publication No. US20020187946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003003
 ; CURRENT APPLICATION NUMBER: US/09/201,936
 ; CURRENT FILING DATE: 1998-12-01
 ; EARLIER APPLICATION NUMBER: 09/011,356
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 2540
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (2540)....(2540)
 ; OTHER INFORMATION: N may be any nucleotide
 US-09-201-936-3

Query Match 100.0%; Score 198; DB 9; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TATGAAGCAGGATCTTTTCTTTGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 60
 Db 826 TATGAAGCAGGATCTTTTCTTTGGACATGATATCTCAGTTAAACAAGGAGCAGCTT 885
 Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
 Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945
 Qy 121 GGAGGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 Db 946 GGAGGGCTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
 Qy 181 CCAGGGTGCAAAATATCTG 198

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
4192.299 Million cell updates/sec

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Searched: 3407233 seqs, 2561960514 residues
Total number of hits satisfying chosen parameters: 6814466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	1588	13	US-10-024-433-3
2	198	100.0	1659	16	US-10-305-720-1053
3	198	100.0	2404	9	US-09-964-899-38
4	198	100.0	2540	9	US-09-201-936-3
5	198	100.0	2540	15	US-10-007-926A-274
6	198	100.0	2540	15	US-10-366-307-1
7	198	100.0	2540	15	US-10-388-360-331
8	198	100.0	2540	16	US-10-641-643-900
9	198	100.0	2540	17	US-10-636-065-218
10	198	100.0	2540	17	US-10-600-272-3
11	198	100.0	3000	17	US-10-636-065-231
12	198	100.0	5232	9	US-09-974-592-3

13	173	87.4	2100	9	US-09-201-936-9	Sequence 9, Appli
14	173	87.4	2100	17	US-10-636-065-224	Sequence 22, App
15	173	87.4	2100	17	US-10-600-272-9	Sequence 9, Appli
16	169.8	85.8	2691	9	US-09-974-592-9	Sequence 9, Appli
17	166	83.8	1758	16	US-10-343-115-1	Sequence 1, Appli
18	166	83.8	1758	16	US-10-343-115-1	Sequence 3, Appli
19	164.4	83.0	1559	13	US-10-024-433-1	Sequence 1, Appli
20	157.8	79.7	152331	13	US-10-095-407-17	Sequence 16, Appli
c 21	131.4	66.4	176373	13	US-10-095-407-17	Sequence 17, Appli
c 22	96.8	48.9	302	11	US-09-969-034-2480	Sequence 2480, Ap
c 23	78.6	39.7	255	15	US-10-102-524-906	Sequence 906, App
24	78.6	39.7	2563	16	US-10-305-720-1076	Sequence 1076, Ap
25	78.6	39.7	2601	15	US-10-641-643-894	Sequence 894, App
26	78.6	39.7	2676	9	US-09-201-936-5	Sequence 3, Appli
27	78.6	39.7	2676	17	US-10-636-065-220	Sequence 220, App
28	78.6	39.7	2676	17	US-10-600-272-5	Sequence 5, Appli
29	78.6	39.7	2916	16	US-10-240-425-1436	Sequence 1436, Ap
30	78.6	39.7	2916	16	US-10-776-827-31	Sequence 31, Appli
31	78.6	39.7	3076	9	US-09-954-456-1635	Sequence 1635, Ap
32	78.6	39.7	3076	14	US-10-197-290-1	Sequence 1, Appli
33	78.6	39.7	3076	15	US-10-388-263-157	Sequence 157, App
34	78.6	39.7	3076	15	US-10-141-618-5	Sequence 11, Appli
35	78.6	39.7	3076	15	US-10-269-909-5	Sequence 5, Appli
36	78.6	39.7	3165	15	US-10-172-118-564	Sequence 5, Appli
37	78.6	39.7	3165	15	US-10-366-307-5	Sequence 564, App
38	78.6	39.7	3165	16	US-10-342-887-564	Sequence 564, App
39	78.6	39.7	3165	15	US-10-353-461-7	Sequence 7, Appli
40	78.6	39.7	3165	15	US-09-971-392-253	Sequence 253, App
41	78.6	39.7	3734	15	US-10-247-671-18	Sequence 18, Appli
42	78.6	39.7	3734	15	US-09-974-592-5	Sequence 5, Appli
43	78.6	39.7	5844	10		
44	78.6	39.7	5857	9		
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ALIGNMENTS

RESULT 1
US-10-024-433-3
; Sequence 3, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-024-433-3

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Best Local Similarity	100.0%	Pred. No.	1.5e-54				
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Gaps	0						
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DB	826	TATGAAGCAGCGATCTTTTACTTTTGGACATGATATCTCAGTTAACAGGACGAGCTT	885				
QY	61	GCAAGAGCTGGATTTTATGCTTTAGCTTAAAGTAAAGTCTTCTACTCTGGA	120				
DB	886	GCAAGAGCTGGATTTTATGCTTTAGCTTAAAGTAAAGTCTTCTACTCTGGA	945				
QY	121	GGAGGGCTAACTGATTGGAGCCCGAGTGAAGCCCTTGGGAAACAATCGTAT	180				

GenCore version 5.1.6
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Title: US-09-654-743-51

Perfect score: 198

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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	198	100.0	2100	6	AR302739	Sequence
2	198	100.0	2100	6	AR435474	Sequence
3	198	100.0	2100	6	AR451574	Sequence
4	198	100.0	2100	6	AR473584	Sequence
5	198	100.0	2100	6	AX412124	Sequence
6	194.8	98.4	2691	6	AR106400	Sequence
7	194.8	98.4	2691	6	AR116702	Sequence
8	194.8	98.4	2691	6	BD190871	Detection
9	194.8	98.4	2691	6	AR370620	Sequence
10	194.8	98.4	2691	6	AX670906	Sequence
11	194.8	98.4	2691	10	MMU88990	U88990 Mus musculus
12	186.8	94.3	1988	10	MMU36842	U36842 Mus musculus
13	185.2	93.5	179719	10	AC137152	AC137152 Mus musculus
14	185.2	93.5	205211	2	AC109227	AC109227 Mus musculus
15	182	91.9	1491	10	AF183429	AF183429 Rattus no
16	182	91.9	2468	10	AB033366	AB033366 Rattus no
17	182	91.9	2032	10	AF304334	AF304334 Rattus no
18	180.4	91.1	2032	10	AF304333	AF304333 Rattus no
19	173	87.4	1588	6	AR263641	Sequence

20	173	87.4	1659	6	E31042	E31042 Method for
21	173	87.4	1659	6	AR270490	AR270490 Sequence
22	173	87.4	1659	9	HSU32974	U32974 Human IAP-1
23	173	87.4	2086	9	BC032729	BC032729 Homo sapi
24	173	87.4	2404	6	CQ714226	CQ714226 Sequence
25	173	87.4	2404	6	AX429575	AX429575 Sequence
26	173	87.4	2540	6	AR103281	AR103281 Sequence
27	173	87.4	2540	6	CQ789350	CQ789350 Sequence
28	173	87.4	2540	6	AR302736	AR302736 Sequence
29	173	87.4	2540	6	AR380355	AR380355 Sequence
30	173	87.4	2540	6	AR435471	AR435471 Sequence
31	173	87.4	2540	6	AR451571	AR451571 Sequence
32	173	87.4	2540	6	AR473581	AR473581 Sequence
33	173	87.4	2540	6	AX412118	AX412118 Sequence
34	173	87.4	2540	6	AX587804	AX587804 Sequence
35	173	87.4	2540	9	HSU45880	U45880 Human X-lin
36	173	87.4	3000	6	AR451578	AR451578 Sequence
37	173	87.4	3000	6	AX412131	AX412131 Sequence
38	173	87.4	5232	6	AR106397	AR106397 Sequence
39	173	87.4	5232	6	AR116699	AR116699 Sequence
40	173	87.4	5232	6	BD190868	BD190868 Detection
41	173	87.4	5232	6	AR370617	AR370617 Sequence
42	173	87.4	5232	6	AX670900	AX670900 Sequence
43	157	79.3	1088	6	CQ734077	CQ734077 Sequence
44	157	79.3	1752	6	AX104956	AX104956 Sequence
45	157	79.3	1752	9	AF164681	AF164681 Homo sapi

ALIGNMENTS

RESULT 1	AR302739	Sequence 9	2100 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	AR302739	Sequence 9	from patent US 6541457.			
DEFINITION	AR302739					
ACCESSION	AR302739					
VERSION	AR302739.1	GI:31691182				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 2100)					
AUTHORS	Korneluk, R.G., MacKenzie, A.E., Baird, S. and Liston, P.					
TITLE	Mammalian IAP gene family, primers, probes and detection methods					
JOURNAL	Patent: US 6541457-A 9 01-APR-2003;					
FEATURES	Location/Qualifiers					
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Query Match	100.0%	Score 198;	DB 6;	Length 2100;
Best Local Similarity	100.0%;	Pred. No. 1.5e-45;		
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QY	1	TATGAAGCACGATCGTTTACTTTTGGAAACATGGATATCTCAGTTAAACAGGACGCTT	60	
Db	916	TATGAAGCACGATCGTTTACTTTTGGAAACATGGATATCTCAGTTAAACAGGACGCTT	975	
QY	61	GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGATTAAGTGAAGTGTTCACGTGTGGA	120	
Db	976	GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGATTAAGTGAAGTGTTCACGTGTGGA	1035	
QY	121	GGAGGGCTCAGGATTTGGAAGCCCAAGCCCTGGGACCGATGAGCCCTGGGACCGATGCTAAGTGCTAC	180	
Db	1036	GGAGGGCTCAGGATTTGGAAGCCCAAGCCCTGGGACCGATGAGCCCTGGGACCGATGCTAAGTGCTAC	1095	
QY	181	CCAGGGTGCATAATACCTTA	198	
Db	1096	CCAGGGTGCATAATACCTTA	1113	

RESULT 2

AR435474
LOCUS AR435474 2100 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6656704.
ACCESSION AR435474
VERSION AR435474.1 GI:40198325
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2100)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE Mammalian apoptosis inhibitor protein gene family, primers, probes and detection methods
JOURNAL Patent: US 6656704-A 9 02-DEC-2003;
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Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTCAGTTAAAGGAGCAGCTT 60
DB 916 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTCAGTTAAAGGAGCAGCTT 975
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 976 GCNAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 180
DB 1036 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 1095
QY 181 CCAGGGTGCATAATACCTA 198
DB 1096 CCAGGGTGCATAATACCTA 1113
RESULT 3
AR451574
LOCUS AR451574 2100 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 224 from patent US 6673917.
ACCESSION AR451574
VERSION AR451574.1 GI:42682599
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2100)
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iAP nucleic acids and uses thereof
JOURNAL Patent: US 6673917-A 224 06-JAN-2004;
FEATURES
Location/Qualifiers
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/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTCAGTTAAAGGAGCAGCTT 60
DB 916 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTCAGTTAAAGGAGCAGCTT 975
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 976 GCNAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 180
DB 1036 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 1095
QY 181 CCAGGGTGCATAATACCTA 198
DB 1096 CCAGGGTGCATAATACCTA 1113
RESULT 5
AR412124
LOCUS AR412124 2100 bp DNA linear PAT 15-JUN-2002
DEFINITION Sequence 224 from Patent WO0226968.
ACCESSION AR412124
VERSION AR412124.1 GI:21444584
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 224 04-APR-2002;
FEATURES
Location/Qualifiers
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ORIGIN

QY 121 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 180
DB 1036 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 1095
QY 181 CCAGGGTGCATAATACCTA 198
DB 1096 CCAGGGTGCATAATACCTA 1113
RESULT 4
AR473584
LOCUS AR473584 2100 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9 from patent US 6689562.
ACCESSION AR473584
VERSION AR473584.1 GI:42711909
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2100)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE Mammalian IAP gene family, primers, probes and detection methods
JOURNAL Patent: US 6689562-A 9 10-FEB-2004;
FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTCAGTTAAAGGAGCAGCTT 60
DB 916 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTCAGTTAAAGGAGCAGCTT 975
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 976 GCNAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 180
DB 1036 GGAGGGCTCACGATGGAAGCCCAAGTGAAGACCCCTGGACACGATGCTTAAGTCTGCTAC 1095
QY 181 CCAGGGTGCATAATACCTA 198
DB 1096 CCAGGGTGCATAATACCTA 1113
RESULT 5
AR412124
LOCUS AR412124 2100 bp DNA linear PAT 15-JUN-2002
DEFINITION Sequence 224 from Patent WO0226968.
ACCESSION AR412124
VERSION AR412124.1 GI:21444584
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 224 04-APR-2002;
FEATURES
Location/Qualifiers
1..2100
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
ORIGIN

Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATACCTAGTTTAAACAGGAGCAGCTT 60
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Db 1461 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATACCTAGTTTAAACAGGAGCAGCTT 1520
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QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
|||||
Db 1521 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1580
|||||

QY 121 GGAGGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
|||||
Db 1581 GGAGGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640
|||||

QY 181 CCAGGGTGCATAATACCTA 198
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Db 1641 CCAGGGTGCATAATACCTA 1658
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RESULT 9
AR370620
LOCUS 2691 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 9 from patent US 6300492.
ACCESSION AR370620
VERSION AR370620.1 GI:34607376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Teang, B.K. and Pratt, C.
TITLE Modulation of IAPs for the diagnosis and antisense treatment of proliferative disease
JOURNAL Patent: US 6300492-A 9 09-OCT-2001;
FEATURES Location/Qualifiers
source 1..2691
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 99.0%; Pred. No. 1.1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1461 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATACCTAGTTTAAACAGGAGCAGCTT 1520
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QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
|||||
Db 1521 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1580
|||||

QY 121 GGAGGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
|||||
Db 1581 GGAGGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640
|||||

QY 181 CCAGGGTGCATAATACCTA 198
|||||
Db 1641 CCAGGGTGCATAATACCTA 1658
|||||

RESULT 10
AX670906
LOCUS 2691 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 9 from Patent EP1277836.
ACCESSION AX670906
VERSION AX670906.1 GI:29329409
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Korneluk, R., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B. and Pratt, C.
TITLE Modulation of the IAPs and naip for the treatment of proliferative diseases
JOURNAL Patent: EP 1277836-A 9 22-JAN-2003;
FEATURES Location/Qualifiers
source 1..2691
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATACCTAGTTTAAACAGGAGCAGCTT 60
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Db 1461 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATACCTAGTTTAAACAGGAGCAGCTT 1520
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
|||||
Db 1521 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1580
|||||

QY 121 GGAGGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
|||||
Db 1581 GGAGGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640
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QY 181 CCAGGGTGCATAATACCTA 198
|||||
Db 1641 CCAGGGTGCATAATACCTA 1658
|||||

RESULT 11
MMU88990
LOCUS 2691 bp mRNA linear ROD 31-MAY-1997
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.
ACCESSION U88990
VERSION U88990.1 GI:2138318
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and MacKenzie, A.E.
TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and MacKenzie, A.E.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
FEATURES Location/Qualifiers
source 1..2691
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/chromosome="X"
/map="A3-A5 region"
/dev_stage="embryo"
gene 1..2691
/gene="miap-3"
exon <1..1545
/gene="miap-3"
/number=1
672..2162
/gene="miap-3"
/note="MIAP-3"

* of the gaps between them are based on estimates that have
 * provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and
 * the accession number will be preserved.

* 1 202770: contig of 202770 bp in length

* 202771 202870: gap of unknown length

* 202871 205211: contig of 2341 bp in length.

FEATURES

source

1. .205211

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

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/clone="RP23-396C19"

/clone_lib="RPCI-23 Female Mouse BAC"

ORIGIN

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 Best Local Similarity 96.0%; Pred. No. 2.9e-42;
 Matches 190; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGGATCGTTACTTTTGGAAACATGGATATCTCAGTTAACAGGAGCAGCTT 60
 Db 43540 TATGAAGCAGGATCGTTACTTTTGGAAACATGGATATCTCAGTTAACAGGAGCAGCTT 43481
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGCCTTCACTGTGGA 120
 Db 43480 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGCCTTCACTGTGGA 120
 QY 121 GGAGGCTCACGGATTGGAAAGCAAGTGAAGACCCCTGGGACCAGCATCTAAGTGCTAC 180
 Db 43420 GGAGGCTCACGGATTGGAAAGCAAGTGAAGACCCCTGGGACCAGCATCTAAGTGCTAC 180
 QY 181 CCAGGCTGCAATACCTA 198
 Db 43360 CCAGGCTGCAATACCTA 43343

RESULT 15

AF183429

LOCUS

AF183429 1491 bp mRNA linear ROD 16-JUL-2002

DEFINITION Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete

cds.

ACCESSION AF183429

VERSION AF183429.1 GI:10765280

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus

1 (bases 1 to 1491)

Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.

Cloning and characterization of the rat homologues of the Inhibitor

of Apoptosis protein 1, 2, and 3 genes

BMC Genomics 3 (1), 5 (2002)

11860601

2 (bases 1 to 1491)

Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.

Direct Submission

Submitted (08-SEP-1999) Department of Biochemistry, Microbiology

and Immunology, University of Ottawa, 451 Smyth Road, Ottawa,

Ontario K1H 8M5, Canada

Location/Qualifiers

1. .1491

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

1. .1491

/note="RIAP-3; similar to X-linked IAP (XIAP)"

/codon_start=1

CDS

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 /protein_id="AAG22969.1"
 /db_xref="GI:10765281"
 /translation="MTFNSFSGSRVTVPADTNKDEEFVEFNLKTFANFPSSPYSA
 STLARAGFLYTGEGDTVQCFSCAAVDRWQYGDVAVGRHRRISVNCRFPNGFYFENG
 TOSTSPGIONQYKSENCVGNRNFALDRPSETHADYLLRTGQVVDISDTIYPRNFM
 CSERAPKTFQNWEDYAHLSPRELAGSLYYTGDIDQVQCFCCGKLKNWPCDRAMS
 EHRHPNCFVFLGRNVNVRSGVSSDRNPNSTNSPRNPAMAEYDARIVTFTGWL
 SVNKEQLARAGFYALGEGDKVCFHCGGLTDWPKSEDPEWQAKWPGVCKYLLDKG
 QEYINNHLTHSLGESVVRTEKTPSVTKIDDTIFQNMVQEAIEWGFNFKDIKTM
 EEKLOTSGSNYLSLEVLIALDLYSAOKNSQDESSQTSLOKDISTEQLRLQBEKLUK
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ORIGIN

Query Match 91.9%; Score 182; DB 10; Length 1491;
 Best Local Similarity 94.9%; Pred. No. 5.4e-41;
 Matches 188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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 Db 790 TATGAAGCAGGATCGTTACTTTTGGAAACATGGATATCTCAGTTAACAGGAGCAGCTT 849
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGCCTTCACTGTGGA 120
 Db 850 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGCCTTCACTGTGGA 120
 QY 121 GGAGGCTCACGGATTGGAAAGCAAGTGAAGACCCCTGGGACCAGCATCTAAGTGCTAC 180
 Db 910 GGAGGCTCACGGATTGGAAAGCAAGTGAAGACCCCTGGGACCAGCATCTAAGTGCTAC 180
 QY 181 CCAGGCTGCAATACCTA 198
 Db 970 CCAGGCTGCAATACCTA 987

Search completed: October 22, 2004, 21:14:32

Job time : 1487.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 19:31:13 ; Search time 261 Seconds

(without alignments)

3982.319 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgatcggttac.....accagggtgcaataacctta 198

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	198	100.0	2100	2	AAT70839	Aat70839 Mouse apo
2	198	100.0	2100	6	ABK93872	Abk93872 Mouse cDN
3	194.8	98.4	2691	2	AAV55041	Aav55041 Murine XI
4	194.8	98.4	2691	8	ABZ58102	Abz58102 Mouse inh
5	186.8	94.3	1988	2	AAT72710	Aat72710 Mouse inh
6	173	87.4	1588	6	ABS52803	AbS52803 DNA encod
7	173	87.4	1659	3	Az448862	Aaz448862 Human XIA
8	173	87.4	1659	10	ACA56455	AcA56455 Human sig
9	173	87.4	1659	12	ADI56251	Adi56251 Human pol
10	173	87.4	2540	6	AAK99405	Aak99405 DNA of AP
11	173	87.4	2540	2	AAT70836	Aat70836 Human apo
12	173	87.4	2540	3	AA64901	Aa64901 Human X-1
13	173	87.4	2540	6	ABK93869	Abk93869 Human cDN
14	173	87.4	2540	6	ABV94283	Abv94283 Breast ca
15	173	87.4	2540	8	AAL53731	Aal53731 X-linked
16	173	87.4	2540	8	AA49663	Ad49663 Human X-1
17	173	87.4	2540	9	ADB81002	AdB81002 RING-SH c
18	173	87.4	2540	10	ADG89383	Adg89383 Cancer de
19	173	87.4	2540	11	ADI31574	Adi31574 Human cDN
20	173	87.4	2540	12	ADH74638	Adh74638 DNA encod
21	173	87.4	2540	12	ADL70165	Adl70165 Human X c

22	173	87.4	3000	6	ABK93875	Abk93875 Human cDN
23	173	87.4	5232	2	AAV55038	Aav55038 Human XIA
24	157	79.3	1752	4	AAD03575	Aad03575 Human IAP
25	149	75.3	1758	6	ABK14678	Abk14678 Human Inh
26	149	75.3	1758	6	ABK14677	Abk14677 Human Inh
27	149	75.3	4993	4	AAD03581	Aad03581 Human IAP
28	147.4	74.4	711	3	AAA06940	Aaa06940 DNA encod
29	147.4	74.4	1559	6	ABK13197	Abk13197 Human tes
30	147.4	74.4	1559	6	ABS52802	AbS52802 DNA encod
31	145.8	73.6	711	4	AAD03582	Aad03582 Chimpanze
32	144.2	72.8	711	4	AAD03583	Aad03583 Gorilla I
33	134.4	67.9	578	2	AAZ02960	Aaz02960 Human IL-
34	109.6	55.4	802	2	AAZ02960	Aaz02960 Human IL-
35	79.8	40.3	1402	2	AAZ03018	Aaz03018 Human IL-
36	77.8	39.3	302	6	ABQ58785	Abq58785 Human col
37	76	38.4	1448	12	ADO26591	Ado26591 cDNA enco
38	76	38.4	2563	9	ADB80989	AdB80989 RING-SH c
39	76	38.4	2563	10	ACA56478	AcA56478 Human sig
40	76	38.4	2563	11	ADI31568	Adi31568 Human cDN
41	76	38.4	2563	12	ADI56274	Adi56274 Human pol
42	76	38.4	2601	2	AAT61591	Aat61591 Human c-I
43	76	38.4	2666	2	AAT70837	Aat70837 Human apo
44	76	38.4	2676	6	ABK93870	Abk93870 Human cDN
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ALIGNMENTS

RESULT 1
AAT70839
ID AAT70839 standard; cDNA; 2100 BP.
XX
AC AAT70839;
XX
DT 02-SEP-1997 (first entry)
XX
DE Mouse apoptosis inhibitor m-xiap cDNA.
XX
KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
KW HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 127..1617
FT /*tag= a
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB001022.
XX
PR 04-AUG-1995; 95US-00511485.
PR 22-DEC-1995; 95US-00576956.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Mackenzie AE, Baird S, Liston P;
XX
DR WPI; 1997-154262/14.
XX
DR P-PSDB; AAW19584.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.
XX
PS Claim 11; Page 78-79; 219pp; English.
XX
CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2

CC genes (AA70836-41) respectively code for a new class of mammalian
 CC proteins (AA19591-86) that are inhibitors of apoptosis (IAP). The murine
 CC xiap gene (for X-linked IAP gene) sequence was constructed from 12
 CC overlapping clones isolated from a mouse embryo lambda-gt11 cDNA library
 CC and from a mouse FIX II genomic library using human xiap cDNA as probe.
 CC IAP nucleic acids can be used to express IAP polypeptides in cells and
 CC animals to inhibit apoptosis, and as primers and probes to identify and
 CC isolate additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy)
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 2; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 2.4e-58;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATCGATATATCTCAGTTAAACAAGGAGCAGCTT 60
 Db 916 TATGAGCAGCGATCGTTACTTTTGGACATCGATATATCTCAGTTAAACAAGGAGCAGCTT 975
 QY 61 GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 120
 Db 976 GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 1035
 QY 121 GGAGGGCTCAGGATTTGGAGCCAAAGTGAAGACCCCTGGGACGAGCATCTAAGTGCTAC 180
 Db 1036 GGAGGGCTCAGGATTTGGAGCCAAAGTGAAGACCCCTGGGACGAGCATCTAAGTGCTAC 1095
 QY 181 CCAGGGTGCAAAATACCTA 198
 Db 1096 CCAGGGTGCAAAATACCTA 1113
 RESULT 2
 ABK93872
 ID ABK93872 standard; cDNA; 2100 BP.
 XX
 AC ABK93872;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.
 XX
 KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Mus sp.
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI; 2002-479562/51.
 XX
 DR P-PSDB; ABG65666.
 XX
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 FT diseases.
 XX
 XX Disclosure; Fig 4; 135pp; English.
 PS

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC cDNA sequence
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 6; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 2.4e-58;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATCGATATATCTCAGTTAAACAAGGAGCAGCTT 60
 Db 916 TATGAGCAGCGATCGTTACTTTTGGACATCGATATATCTCAGTTAAACAAGGAGCAGCTT 975
 QY 61 GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 120
 Db 976 GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 1035
 QY 121 GGAGGGCTCAGGATTTGGAGCCAAAGTGAAGACCCCTGGGACGAGCATCTAAGTGCTAC 180
 Db 1036 GGAGGGCTCAGGATTTGGAGCCAAAGTGAAGACCCCTGGGACGAGCATCTAAGTGCTAC 1095
 QY 181 CCAGGGTGCAAAATACCTA 198
 Db 1096 CCAGGGTGCAAAATACCTA 1113
 RESULT 3
 AAV55041
 ID AAV55041 standard; cDNA; 2691 BP.
 XX
 AC AAV55041;
 XX
 DT 13-NOV-1998 (first entry)
 XX
 DE Murine XIAP coding sequence.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 CDS 672..2162
 FT /*tag= a
 FT /product= "XIAP"
 FT
 XX WO9835693-A2.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98WO-1B000781.
 XX
 PR 13-FEB-1997; 97US-00800929.
 XX
 PA (UYOT-) UNIV OTTAWA.
 XX
 XX

PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 XX WPI; 1998-467164/40.
 DR P-PSDB; AAW69297.
 XX
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
 PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX
 XX Claim 13; Fig 4; 147pp; English.
 PS
 XX This sequence encodes the mouse XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 XX
 SQ Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 U; 0 Other;
 Query Match 98.4%; Score 194.8; DB 2; Length 2691;
 Best Local Similarity 99.0%; Pred. No. 3.5e-57;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGCATCGTTACTTTTGGACATGATATCTAGTTAAACAGAGCAGCTT 60
 Db |||||||
 QY 1461 TATGAAGCAGCATCGTTACTTTTGGACATGATATCTAGTTAAACAGAGCAGCTT 1520
 Db |||||||
 QY 61 GCAAGAGCTGGATTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGTTCACCTGTGGA 120
 Db |||||||
 QY 1521 GCAAGAGCTGGATTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGTTCACCTGTGGA 1580
 Db |||||||
 QY 121 GGAGGGCTCAGGATTGAAGCAAGTGAAGACCCCTGGGACCATGCTAAAGTGTCTAC 180
 Db |||||||
 QY 1581 GGAGGGCTCAGGATTGAAGCAAGTGAAGACCCCTGGGACCATGCTAAAGTGTCTAC 1640
 Db |||||||
 QY 181 CCAGGGTGCAAAATACCTA 198
 Db |||||||
 QY 1641 CCAGGGTGCAAAATACCTA 1658
 Db |||||||
 RESULT 4
 ABZ58102
 ID ABZ58102 standard; cDNA; 2691 BP.
 AC ABZ58102;
 XX
 XX 22-APR-2003 (first entry)
 DT
 XX
 XX Mouse inhibitor of apoptosis protein MIAP3 cDNA.
 DE
 XX Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukaemia;
 KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy;
 KW gene; ss.
 XX
 XX Mus sp.
 OS
 XX Location/Qualifiers
 FH 672..2162
 FT CDS /*tag= a
 FT /*product= "MIAP3"
 FT
 XX
 XX W02003004606-A2.

PD 16-JAN-2003.
 XX
 XX 03-JUL-2002; 2002WO-US021002.
 PF
 XX
 XX 03-JUL-2001; 2001US-00898158.
 PR
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX
 XX Troy CM, Shelanski ML;
 PI
 XX
 XX WPI; 2003-210351/20.
 DR P-PSDB; ABP72157.
 DR
 XX
 XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 PT treating cancer, neurodegenerative disorder or cardiomyopathy.
 PT
 XX
 XX Disclosure; Fig 15B; 124pp; English.
 PS
 XX The present sequence is that of cDNA encoding murine inhibitor of
 CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as
 CC an antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,
 CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
 CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and equamous cell carcinoma (all claimed)
 XX
 SQ Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 U; 0 Other;
 Query Match 98.4%; Score 194.8; DB 8; Length 2691;
 Best Local Similarity 99.0%; Pred. No. 3.5e-57;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGCATCGTTACTTTTGGACATGATATCTAGTTAAACAGAGCAGCTT 60
 Db |||||||
 QY 1461 TATGAAGCAGCATCGTTACTTTTGGACATGATATCTAGTTAAACAGAGCAGCTT 1520
 Db |||||||
 QY 61 GCAAGAGCTGGATTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGTTCACCTGTGGA 120
 Db |||||||
 QY 1521 GCAAGAGCTGGATTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGTTCACCTGTGGA 1580
 Db |||||||
 QY 121 GGAGGGCTCAGGATTGAAGCAAGTGAAGACCCCTGGGACCATGCTAAAGTGTCTAC 180
 Db |||||||
 QY 1581 GGAGGGCTCAGGATTGAAGCAAGTGAAGACCCCTGGGACCATGCTAAAGTGTCTAC 1640
 Db |||||||
 QY 181 CCAGGGTGCAAAATACCTA 198
 Db |||||||
 QY 1641 CCAGGGTGCAAAATACCTA 1658
 Db |||||||
 RESULT 5
 AAT72710
 ID AAT72710 standard; DNA; 1988 BP.
 AC AAT72710;
 XX
 XX 16-SEP-1997 (first entry)
 DT
 XX
 XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
 DE
 XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
 KW degenerative disease; infectious disease; autoimmune disease; cancer;
 KW gene therapy; diagnosis; ss.
 XX
 XX Mus musculus.
 OS
 XX Location/Qualifiers
 FH 212..1702
 FT CDS /*tag= a
 FT

XX W09723501-A1.
 PN
 XX
 XX
 XX 03-JUL-1997.
 XX
 XX 20-DEC-1996; 96WO-AU000827.
 PF
 XX
 XX 22-DEC-1995; 95AU-00007275.
 PR
 XX
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA
 XX
 XX Vaux DL;
 PI
 XX
 XX WPI; 1997-350966/32.
 DR
 XX P-PSDB; AAW19745.
 DR
 XX Isolated protein homologues of viral inhibitors of apoptosis - used to
 PT modulate apoptosis for treatment of degenerative, infectious or
 PT auto-immune diseases and cancer.
 PT
 PS Claim 24; Page 44-47; 136pp; English.
 PS
 XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
 CC homologue A (MHA) (AAW19745), a murine homologue of baculovirus
 CC inhibitor of apoptosis protein (IAP). It was isolated from a mouse liver
 CC cDNA library on the basis of homology to Orgyia pseudotsuguta
 CC polyhedrosis virus IAP BIR and KING finger amino acid motifs. Animal IAP
 CC homologue nucleic acids (see also AAT72711-17) can be used to produce
 CC polypeptides useful in methods for modulating apoptosis in animal cells,
 CC specifically for treatment, by inhibition, of degenerative and infectious
 CC disease or, by promotion, of cancer and autoimmune disease, and can be
 CC used for gene therapy of these diseases
 XX
 XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 U; 0 Other;
 SQ
 Query Match 94.3%; Score 186.8; DB 2; Length 1988;
 Best Local Similarity 96.5%; Pred. No. 1.9e-54;
 Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATATCTCAGTTTAAAGGAGCAGCTT 60
 Db 1001 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATATCTCAGTTTAAAGGAGCAGCTT 1060
 QY 61 GCAAGAGCTGGATTTATGCTTTTGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 120
 Db 1061 GCAAGAGCTGGATTTATGCTTTTGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 1120
 QY 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTAAAGTGTCTAC 180
 Db 1121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTAAAGTGTCTAC 1180
 QY 181 CCAGGGTGCAAAATACCTA 198
 Db 1181 CCAGGGTGCAAAATACCTA 1198
 RESULT 6
 ABS52803
 ID ABS52803 standard; DNA; 1588 BP.
 XX
 XX ABS52803;
 AC
 XX
 XX 15-NOV-2002 (first entry)
 DT
 XX DNA encoding X-linked inhibitor of apoptosis, XIAP.
 DE
 XX Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; TIAP;
 KW fertility; testicular cancer; male infertility; male birth control;
 KW X-linked inhibitor of apoptosis; gene; ds.
 XX
 XX Mammalia.
 OS
 XX
 XX Key Location/Qualifiers
 FH

FT CDS 34..1527
 FT /tag= a
 FT /transl_except= (pos:34..36, aa:Xaa)
 FT /product= "X-linked inhibitor of apoptosis protein, XIAP"
 FT /partial
 FT /note= "Start codon illegible in specification;
 represented as nnn"
 XX
 PN US2002086409-A1.
 XX
 XX 04-JUL-2002.
 PD
 XX
 XX 18-DEC-2001; 2001US-00024433.
 PF
 XX 29-JAN-1998; 98US-0073001P.
 PR
 XX 29-JAN-1999; 99US-00239867.
 PR
 XX (KORN/) KORNELUK R G.
 PA (LAGA/) LAGACE M.
 PA
 XX Korneluk RG, Lagace M;
 PI
 XX WPI; 2002-642245/69.
 DR P-PSDB; ABG32418.
 DR
 XX Novel polypeptide, a member of inhibitor of apoptosis family of proteins
 PT that is expressed in testes useful for modulating apoptosis in cells,
 PT particular cells involved in male fertility.
 PT
 PS Example 3; Fig 4A; 24pp; English.
 PS
 XX A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
 CC apoptosis) family of proteins that is expressed in the testes. (I) is
 CC useful for identifying a compound that modulates TIAP biological activity
 CC (I) is useful for increasing apoptosis in a cell, preferably a germ-line
 CC cell and for increasing fertility in an animal. (I) is useful for
 CC treating or preventing apoptosis which occurs as a part of testicular
 CC cancer and male infertility. TIAP may be manipulated for use as a male
 CC birth control. TIAP polypeptides and nucleic acid sequences also have
 CC diagnostic use in the detection or monitoring of conditions involving
 CC aberrant levels of apoptosis. The present sequence represents the coding
 CC sequence of X-linked inhibitor of apoptosis (XIAP)
 XX
 SQ Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;
 Query Match 87.4%; Score 173; DB 6; Length 1588;
 Best Local Similarity 92.4%; Pred. No. 1.2e-49;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATATCTCAGTTTAAAGGAGCAGCTT 60
 Db 826 TATGAAGCAGGATCGTTACTTTTGGAAACATGATATATCTCAGTTTAAAGGAGCAGCTT 885
 QY 61 GCAAGAGCTGGATTTATGCTTTTGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 120
 Db 886 GCAAGAGCTGGATTTATGCTTTTGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 945
 QY 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTAAAGTGTCTAC 180
 Db 946 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTAAAGTGTCTAC 1005
 QY 181 CCAGGGTGCAAAATACCT 197
 Db 1006 CCAGGGTGCAAAATATCT 1022
 RESULT 7
 AAZ48862
 ID AAZ48862 standard; cDNA; 1659 BP.
 XX
 XX AAZ48862;
 AC
 XX
 XX 24-MAR-2000 (first entry)
 DT

XX DE Human XIAP coding sequence.

XX DE Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TAK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; Transforming growth factor-beta; ds.

XX OS Homo sapiens.

XX PN JP11326328-A.

XX PD 26-NOV-1999.

XX PF 13-MAY-1998; 98JP-00130378.

XX PR 13-MAY-1998; 98JP-00130378.

XX PA (MATS/) MATSUMOTO K.

XX DR WPI; 2000-078337/07.

XX DR P-PSDB; AAY59451.

XX PT Screening a substance which inhibits combination of the X-linked inhibitor of apoptosis protein.

XX PS Disclosure; Page 28-30; 43pp; Japanese.

XX CC This sequence encodes the human XIAP protein. The invention relates to a method for screening a substance inhibiting the formation of a complex between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding protein 1 (TAB1) and a substance to be tested are contacted with each other and then the presence or formation of a complex between XIAP and TAB1 is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocyte migration, physiologically active substance induction, immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta (transforming growth factor-beta) type I and/or type II receptor is useful as a drug

XX SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;

Query Match 87.4%; Score 173; DB 3; Length 1659;

Best Local Similarity 92.4%; Pred. No. 1.2e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60

Db 874 TATGAAGCAGCGATCTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 933

Qy 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120

Db 934 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 993

Qy 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCTGAAGTGTAC 180

Db 994 GGAGGGCTCAGTGTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCTGAAGTGTAT 1053

Qy 181 CCAGGGTGCAAAATACCT 197

Db 1054 CCAGGGTGCAAAATATCT 1070

RESULT 8

ACAS6455

ID ACAS6455 standard; cDNA; 1659 BP.

XX AC ACAS6455;

XX DT 06-JUN-2003 (first entry)

XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1053.

XX DE Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX OS Homo sapiens.

XX PN US6500938-B1.

XX PD 31-DEC-2002.

XX PF 30-JAN-1998; 98US-00016434.

XX PR 30-JAN-1998; 98US-00016434.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Au-Young J, Seilhamer JJ;

XX DR WPI; 2003-352189/33.

XX PT Combination of polynucleotide probes, useful as array elements in a microarray for monitoring the expression of a number of target polynucleotides.

XX PS Claim 1; SEQ ID NO 1053; 65pp; English.

XX CC The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=06500938B1

XX SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;

Query Match 87.4%; Score 173; DB 10; Length 1659;

Best Local Similarity 92.4%; Pred. No. 1.2e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60

Db 874 TATGAAGCAGCGATCTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 933

Qy 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120

Db 934 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 993

Qy 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCTGAAGTGTAC 180

Db 994 GGAGGGCTCAGTGTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCTGAAGTGTAT 1053

Qy 181 CCAGGGTGCAAAATACCT 197

Db 1054 CCAGGGTGCAAAATATCT 1070

RESULT 9
 ADI56251
 ID ADI56251 standard; DNA; 1659 BP.
 XX
 AC ADI56251;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human polynucleotide probe #1053.
 XX
 KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
 KW effector-like polypeptide; cancer; immunopathology; neuropathology;
 KW drug development; toxicology; carcinogenicity;
 KW signalling pathway polypeptide; adrenal gland; bladder; bone;
 KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
 KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
 KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
 XX
 OS Homo sapiens.
 XX
 FN US2004010136-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 26-NOV-2002; 2002US-00305720.
 XX
 PR 30-JAN-1998; 98US-00016434.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Seilhamer JJ;
 XX
 DR WPI; 2004-090520/09.
 XX
 PT New composition comprising polynucleotide probes, useful as array
 PT elements in a microarray for monitoring the expression of target
 PT polynucleotides or purifying a subpopulation of mRNAs, cDNAs, or genomic
 PT fragments.
 XX
 PS Claim 6; SEQ ID NO 1053; 73pp; English.
 XX
 CC The invention relates to a composition of polynucleotide probes
 CC comprising first polynucleotide probes comprising at least a portion of a
 CC gene encoding a receptor-like polypeptide, second polynucleotide probes
 CC comprising at least a portion of a gene encoding a transducing
 CC polypeptide and third polynucleotide probes comprising at least a portion
 CC of a gene encoding an effector-like polypeptide. The probes of the
 CC composition are useful as array elements in a microarray for monitoring
 CC the expression of target polynucleotides. The microarray is useful in the
 CC diagnosis and treatment of cancer, an immunopathology or a
 CC neuropathology. It can also be used for drug discovery and development,
 CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
 CC Microarrays can also be used for monitoring the progression of diseases
 CC that may be associated with the altered expression of signalling pathway
 CC polypeptides. The composition can also be used to purify a subpopulation
 CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
 CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
 CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
 CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
 CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
 CC epilepsy, Alzheimer's disease or depression. This sequence represents a
 CC human polynucleotide probe of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
 Query Match 87.4%; Score 173; DB 12; Length 1659;
 Best Local Similarity 92.4%; Pred. No. 1.2e-49;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

1 TATGAAGCACGATCGTTTACTTTTGGAAACATGGATATCTCAGTTTAAACAAGAGCAGCTT 60
 |||||
 874 TATGAAGCACGATCGTTTACTTTTGGAAACATGGATATCTCAGTTTAAACAAGAGCAGCTT 933
 |||||
 61 GCAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120
 |||||
 934 GCAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 993
 |||||
 121 GGAGGGCTCAGGATTGAAGCAAGTGAAGACCCCTGGACCACGATGCTTAAGTGCTAC 180
 |||||
 994 GGAGGGCTCAGGATTGAAGCAAGTGAAGACCCCTGGACCACGATGCTTAAGTGCTAC 1053
 |||||
 181 CCAGGGTGCATAATACCT 197
 |||||
 1054 CCAGGGTGCATAATATCT 1070
 |||||
 RESULT 10
 AAK99405
 ID AAK99405 standard; DNA; 2404 BP.
 XX
 AC AAK99405;
 XX
 DT 27-JUN-2002 (first entry)
 XX
 DE DNA of APP related human homologue hCP35211.
 XX
 KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
 KW amyloid precursor protein; tissue-specific expression control; human APP;
 KW APP pathway modulator; gene therapy; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 692..1528
 FT /*tag= a
 FT /product= "Protein of human homologue hCP35211"
 FT /note= "No start codon"
 XX
 PN WO200226820-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 01-OCT-2001; 2001WO-EP011345.
 XX
 PR 29-SEP-2000; 2000US-0236893P.
 PR 14-JUN-2001; 2001US-0298309P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
 PI Reinhardt MWHM, Zusman S;
 XX
 DR WPI; 2002-315796/35.
 DR P-PSDB; AA020511.
 XX
 XX New transgenic fly, containing DNA encoding an Abeta portion of human
 XX APP, useful for identifying agents which modulate the APP pathway and
 XX which can be used to treat Alzheimer's disease.
 PS Example 4; Page 111; 129pp; English.
 XX
 CC The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-
 CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent

CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC represents the DNA of the APP related human homologue hCP95211
XX
SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;

Query Match 87.4%; Score 173; DB 6; Length 2404;
Best Local Similarity 92.4%; Pred. No. 1.4e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTTGGACATGATATCTACGTTAAACAGGAGCAGCTT 60
DB |||||
QY 827 TATGAAGCAGCGATCTTACTTTTGGACATGATATCTACGTTAAACAGGAGCAGCTT 886
DB |||||
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGGA 120
DB |||||
QY 887 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGGA 946
DB |||||
QY 121 GGAGGGCTCAGCGATTGGAGGCCAAGTGAAGACCCCTGGGACCGAGCATGCTAAGTGTCTAC 180
DB |||||
QY 947 GGAGGGCTAAGTGAAGGCCAAGTGAAGACCCCTGGGACCGAGCATGCTAAGTGTCTAC 180
DB |||||
QY 181 CCAGGGTGCAAAATACCT 197
DB |||||
QY 1007 CCAGGGTGCAAAATATCT 1023
DB |||||

RESULT 11
AAAT70836
ID AAAT70836 standard; cDNA; 2540 BP.
XX
AC AAAT70836;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor xiap cDNA.

KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.

OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 34..1527
FT /*tag= a
XX
XX WO9706255-A2.
XX
XX 20-FEB-1997.
XX
XX 05-AUG-1996; 96WO-IB001022.
XX
XX 04-AUG-1995; 95US-00511485.
XX
XX 22-DEC-1995; 95US-00576956.
XX
XX (UYOT-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
XX WPI; 1997-154262/14.
XX P-PSDB; AAW19581.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
XX inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
XX susceptibility to apoptotic disease.

XX Claim 12; Page 67-68; 219pp; English.
XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2

CC genes (AAAT70836-41) respectively code for a new class of mammalian
CC proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap
CC gene (for X-linked IAP gene) was isolated from a human foetal brain ZapII
CC cDNA library using an X-linked sequence tag site that shows strong
CC homology with the conserved ring zinc finger domain of baculovirus CpiAP
CC and OpIAP genes. The gene was assigned to chromosome Xq25 by FISH. IAP
CC nucleic acids can be used to express IAP polypeptides in cells and
CC animals to inhibit apoptosis, and as primers and probes to identify and
CC isolate additional IAP genes, as well as in methods for treating diseases
CC and disorders involving apoptosis (anti-apoptotic gene therapy)
XX

SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;

Query Match 87.4%; Score 173; DB 2; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.4e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTTGGACATGATATCTACGTTAAACAGGAGCAGCTT 60
DB |||||
QY 826 TATGAAGCAGCGATCTTACTTTTGGACATGATATCTACGTTAAACAGGAGCAGCTT 885
DB |||||
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGGA 120
DB |||||
QY 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGGA 945
DB |||||
QY 121 GGAGGGCTCAGCGATTGGAGGCCAAGTGAAGACCCCTGGGACCGAGCATGCTAAGTGTCTAC 180
DB |||||
QY 946 GGAGGGCTAAGTGAAGGCCAAGTGAAGACCCCTGGGACCGAGCATGCTAAGTGTCTAC 180
DB |||||
QY 181 CCAGGGTGCAAAATACCT 197
DB |||||
QY 1006 CCAGGGTGCAAAATATCT 1022
DB |||||

RESULT 12
AAA64901
ID AAA64901 standard; DNA; 2540 BP.
XX
AC AAA64901;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human X-linked inhibitor of apoptosis DNA.

KW X-linked inhibitor of apoptosis; XIAP; MLIP; U45880; antisense;
KW antiinflammatory; cytostatic; tumour; ds.

OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 34..1527
FT /*tag= a
FT /product= "X-linked inhibitor of apoptosis"

XX US6087173-A.
XX
XX 11-JUL-2000.
XX
XX 09-SEP-1999; 99US-00392580.
XX
XX 09-SEP-1999; 99US-00392580.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsett LM, Ackermann EJ;
XX WPI; 2000-498201/44.
XX P-PSDB; AAY99985.

XX Antisense compound useful for research reagents, diagnostics, prophylaxis
XX and for treating disorders associated with X-linked inhibitor of
XX apoptosis, modulates expression of X-linked inhibitor of apoptosis.

PS Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to

CC inhibit expression of the human X-linked inhibitor of apoptosis. The

CC present sequence is the X-linked inhibitor of apoptosis DNA. Modified

CC phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are more

CC effective inhibitors than unmodified oligonucleotides. The

CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis

CC expression in cells and tissues in vitro. The oligonucleotides are also

CC useful for treating animals or humans, prone to a disease associated with

CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used

CC prophylactically to prevent infection, inflammation or tumour formation

XX

SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 87.4%; Score 173; DB 3; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.4e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAACAAGGAGCGCTT 60

DB 826 TATGAGCAGCGATCTTACTTTTGGACATGGATATCTCAGTTAACAAGGAGCGCTT 885

QY 61 GCAAGAGCTGCGATTTATGCTTTAGTGAAGCGATAAAGTGAAGTGTCCACTGTGGA 120

DB 886 GCAAGAGCTGCGATTTATGCTTTAGTGAAGTGAAGTGAAGTGTCCACTGTGGA 945

QY 121 GGAGGGCTCACGGATTGGAGCCAGTGAAGACCCCTGGGACGAGCATGCTAAGTGTCTAC 180

DB 946 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTGGGACGAGCATGCTAAGTGTCTAT 1005

QY 181 CCAGGTGCAAAATACCT 197

DB 1006 CCAGGTGCAAAATATCT 1022

RESULT 13

ABK93869

ID ABK93869 standard; cDNA; 2540 BP.

XX

AC ABK93869;

XX

DT 26-AUG-2002 (first entry)

XX

DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.

XX

KW Human; ss; gene; antisense; inhibitor of apoptosis; XIAP1; XIAP2; XIAP;

KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;

KW pancreatic cancer; embryonic development; viral pathogenesis;

KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;

KW lupus erythematosus; herpes virus infection; pox virus infection;

KW adenovirus infection; proliferative disease.

XX

OS Homo sapiens.

XX

DN WC200226968-A2.

XX

PD 04-APR-2002.

XX

PF 27-SEP-2001; 2001WO-CA001379.

XX

PR 28-SEP-2000; 2000US-00672717.

XX

PA (UYOT-) UNIV OTTAWA.

XX

PA (AEGE-) AEGERA THERAPEUTICS INC.

XX

PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX

PI WPI; 2002-479562/51.

DR

XX

DR P-PSDB; ABG65663.

XX

PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing

PT apoptosis in a cell, for treating cancer and other proliferative

PT diseases.

XX

PS Disclosure; Fig 1; 135pp; English.

XX

CC The invention relates to an inhibitor of apoptosis (IAP) antisense

CC nucleic acid (I) that inhibits IAP biological activity, regardless of

CC length of the antisense nucleic acid, the IAP proteins may be mouse or

CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical

CC composition comprising a mammalian IAP antisense molecule and a method of

CC enhancing apoptosis in a cell, comprising administering a negative

CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP

CC antisense inhibitor is useful for enhancing apoptosis in a cell in a

CC mammal diagnosed with a proliferative disease. The method is useful for

CC treating a patient diagnosed with a proliferative disease like cancer.

CC The IAP antisense molecule is useful to treat, ameliorate, improve,

CC sustain or prevent proliferative diseases (e.g. ovarian cancer,

CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or

CC conditions where apoptosis is involved or implicated (e.g. embryonic

CC development, viral pathogenesis, autoimmune disorders, neurodegenerative

CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes

CC virus, pox virus and adenovirus). The present sequence is a human IAP

CC cDNA sequence

XX

SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 0 U; 22 Other;

Query Match 87.4%; Score 173; DB 6; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.4e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAACAAGGAGCGCTT 60

DB 826 TATGAGCAGCGATCTTACTTTTGGACATGGATATCTCAGTTAACAAGGAGCGCTT 885

QY 61 GCAAGAGCTGCGATTTATGCTTTAGTGAAGCGATAAAGTGAAGTGTCCACTGTGGA 120

DB 886 GCAAGAGCTGCGATTTATGCTTTAGTGAAGCGCGAGTGAAGTGTCCACTGTGGA 945

QY 121 GGAGGGCTCACGGATTGGAGCCAGTGAAGACCCCTGGGACGAGCATGCTAAGTGTCTAC 180

DB 946 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTGGGACGAGCATGCTAAGTGTCTAT 1005

QY 181 CCAGGTGCAAAATACCT 197

DB 1006 CCAGGTGCAAAATATCT 1022

RESULT 14

ABV94283

ID ABV94283 standard; cDNA; 2540 BP.

XX

AC ABV94283;

XX

DT 08-JAN-2003 (first entry)

XX

DE Breast carcinoma related nucleotide sequence SEQ ID NO:274.

XX

DN Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;

XX

OS ss.

XX

OS Homo sapiens.

XX

PN WC200246467-A2.

XX

PD 13-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-IB002811.

XX

PR 08-DEC-2000; 2000US-0254090P.

XX

PR 07-DEC-2001; 2001US-00007926.

XX

PA (IPSO-) IPSOGEN.

XX

PI Bertucci F, Houlgate R, Birnbaum D, Nguyen C, Viens P, Fert V;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 20:15:23 ; Search time 54 Seconds
(without alignments)
206.226 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgatcggttac.....accagggcgcaataccta 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/ECTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	2100	2	US-08-511-485-9
2	198	100.0	2100	4	US-09-201-936-9
3	198	100.0	2100	4	US-09-011-356-9
4	198	100.0	2100	4	US-09-672-717-224
5	198	100.0	2100	4	US-09-201-932-9
6	194.8	98.4	2691	3	US-09-212-971-9
7	194.8	98.4	2691	3	US-08-800-929A-9
8	194.8	98.4	2691	3	US-09-617-053A-9
9	173	87.4	1588	3	US-09-239-867-3
10	173	87.4	1588	4	US-10-024-433-3
11	173	87.4	1659	4	US-09-016-434-1053
12	173	87.4	2540	2	US-08-511-485-3
13	173	87.4	2540	3	US-09-392-580-1
14	173	87.4	2540	4	US-09-201-936-3
15	173	87.4	2540	4	US-09-023-655-900
16	173	87.4	2540	4	US-09-011-356-3
17	173	87.4	2540	4	US-09-672-717-218
18	173	87.4	2540	4	US-09-201-932-3
19	173	87.4	3000	4	US-09-672-717-231
20	173	87.4	5232	3	US-09-212-971-3
21	173	87.4	5232	3	US-08-800-929A-3
22	173	87.4	5232	3	US-09-617-053A-3
23	147.4	74.4	711	3	US-09-121-979-3
24	147.4	74.4	711	3	US-09-332-319-3
25	147.4	74.4	1559	3	US-09-239-867-1
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27	134.4	67.9	152331	3	US-09-128-155-16

c

28 109.6 55.4 176373 3 US-09-128-155-17 Sequence 17, Appl
29 76 38.4 1448 4 US-09-579-692B-57 Sequence 57, Appl
30 76 38.4 2563 4 US-09-016-434-1076 Sequence 1076, Ap
31 76 38.4 2563 4 US-09-023-655-894 Sequence 894, App
32 76 38.4 2601 3 US-08-569-749-3 Sequence 3, Appli
33 76 38.4 2601 5 PCT-US96-12860-3 Sequence 3, Appli
34 76 38.4 2676 2 US-08-511-485-5 Sequence 5, Appli
35 76 38.4 2676 4 US-09-201-936-5 Sequence 5, Appli
36 76 38.4 2676 4 US-09-011-356-5 Sequence 5, Appli
37 76 38.4 2676 4 US-09-672-717-220 Sequence 220, App
38 76 38.4 2676 4 US-09-201-932-5 Sequence 5, Appli
39 76 38.4 2916 4 US-09-814-915A-31 Sequence 31, Appli
40 76 38.4 3076 2 US-09-205-144-1 Sequence 1, Appli
41 76 38.4 3076 4 US-09-814-915A-11 Sequence 11, Appli
42 76 38.4 3734 4 US-09-579-692B-7 Sequence 7, Appli
43 76 38.4 6669 3 US-09-212-971-5 Sequence 5, Appli
44 76 38.4 6669 3 US-08-800-929A-5 Sequence 5, Appli
45 76 38.4 6669 3 US-09-617-053A-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 100.0%; Score 198; DB 2; Length 2100;
Best Local Similarity 100.0%; Pred. No. 2.9e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 TATGAAGCAGCGATCGTACTTTTGGACATGGTATCTACTACAGGACAGCTT 60
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Db 916 TATGAAGCAGCGATGTTACTTTTGGAACTGATATATCTAGTTAAACAAGGAGCAGCTT 975
Qy 61 GCAAGAGCTGATTTATGCTTTTAGTGAAGCGATAAAGTGAAGTGTTCACCTGTGGA 120
Db 976 GCAAGAGCTGATTTATGCTTTTAGTGAAGCGATAAAGTGAAGTGTTCACCTGTGGA 1035
Qy 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCCAGCATGCTTAAGTGCTAC 180
Db 1036 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCCAGCATGCTTAAGTGCTAC 1095
Qy 181 CCAGGGTGCAATACCTA 198
Db 1096 CCAGGGTGCAATACCTA 1113
RESULT 2
US-09-201-936-9
; Sequence 9, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9
Query Match 100.0%; Score 198; DB 4; Length 2100;
Best Local Similarity 100.0%; Pred. No. 2.9e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATGAAGCAGCGATGTTACTTTTGGAACTGATATATCTAGTTAAACAAGGAGCAGCTT 60
Db 916 TATGAAGCAGCGATGTTACTTTTGGAACTGATATATCTAGTTAAACAAGGAGCAGCTT 975
Qy 61 GCAAGAGCTGATTTATGCTTTTAGTGAAGCGATAAAGTGAAGTGTTCACCTGTGGA 120
Db 976 GCAAGAGCTGATTTATGCTTTTAGTGAAGCGATAAAGTGAAGTGTTCACCTGTGGA 1035
Qy 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCCAGCATGCTTAAGTGCTAC 180
Db 1036 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCCAGCATGCTTAAGTGCTAC 1095
Qy 181 CCAGGGTGCAATACCTA 198
Db 1096 CCAGGGTGCAATACCTA 1113

RESULT 3
US-09-011-356-9
; Sequence 9, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-011-356-9
Query Match 100.0%; Score 198; DB 4; Length 2100;
Best Local Similarity 100.0%; Pred. No. 2.9e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 916 TATGAAGCAGCGATGTTACTTTTGGAACTGATATATCTAGTTAAACAAGGAGCAGCTT 975
Qy 61 GCAAGAGCTGATTTATGCTTTTAGTGAAGCGATAAAGTGAAGTGTTCACCTGTGGA 120
Db 976 GCAAGAGCTGATTTATGCTTTTAGTGAAGCGATAAAGTGAAGTGTTCACCTGTGGA 1035
Qy 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCCAGCATGCTTAAGTGCTAC 180
Db 1036 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCCAGCATGCTTAAGTGCTAC 1095
Qy 181 CCAGGGTGCAATACCTA 198
Db 1096 CCAGGGTGCAATACCTA 1113
RESULT 4
US-09-672-717-224
; Sequence 224, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 224
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-672-717-224
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Best Local Similarity 100.0%; Pred. No. 2.9e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 916 TATGAAGCAGCGATGTTACTTTTGGAACTGATATATCTAGTTAAACAAGGAGCAGCTT 975

QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGA 120
 Db |||||
 QY 976 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGA 1035
 Db |||||
 QY 121 GGAGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGACCCAGCATGCTAAGTGTCTAC 180
 Db |||||
 QY 1036 GGAGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGACCCAGCATGCTAAGTGTCTAC 1095
 Db |||||
 QY 181 CCAGGCTGCAAAATACCTA 198
 Db |||||
 QY 1096 CCAGGCTGCAAAATACCTA 1113
 Db |||||

RESULT 5

US-09-201-932-9
 ; Sequence 9, Application US/09201932A
 ; Patent No. 6689562
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; FILE REFERENCE: 07891/003004
 ; CURRENT APPLICATION NUMBER: US/09/201,932A
 ; EARLIER FILING DATE: 1998-12-01
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 4.0
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 ; LENGTH: 2100
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 ; ORGANISM: Mus musculus
 US-09-201-932-9

Query Match 100.0%; Score 198; DB 4; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 2.9e-61;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGCATCGTTACTTTTGGAAACATGGATATATCTCAGTTTAAACAAGGAGCAGCTT 60
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 QY 916 TATGAAGCAGCATCGTTACTTTTGGAAACATGGATATATCTCAGTTTAAACAAGGAGCAGCTT 975
 Db |||||
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGA 120
 Db |||||
 QY 976 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGA 1035
 Db |||||
 QY 121 GGAGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGACCCAGCATGCTAAGTGTCTAC 180
 Db |||||
 QY 1036 GGAGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGACCCAGCATGCTAAGTGTCTAC 1095
 Db |||||
 QY 181 CCAGGCTGCAAAATACCTA 198
 Db |||||
 QY 1096 CCAGGCTGCAAAATACCTA 1113
 Db |||||

RESULT 6

US-09-212-971-9
 ; Sequence 9, Application US/09212971B
 ; Patent No. 6107041
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; TITLE OF INVENTION: DISEASE
 ; FILE REFERENCE: 07891/009002
 ; CURRENT APPLICATION NUMBER: US/09/212,971B
 ; CURRENT FILING DATE: 1998-12-16
 ; EARLIER FILING DATE: 1996-04-26
 ; EARLIER FILING DATE: 1996-04-26
 ; EARLIER FILING DATE: 1996-03-05, 590
 ; EARLIER FILING DATE: 1996-11-14
 ; EARLIER FILING DATE: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 2691
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-212-971-9

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 Best Local Similarity 99.0%; Pred. No. 4.7e-60;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 QY 1461 TATGAAGCAGCATCGTTACTTTTGGAAACATGGATATATCTCAGTTTAAACAAGGAGCAGCTT 1520
 Db |||||
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGA 120
 Db |||||
 QY 1521 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGA 1580
 Db |||||
 QY 121 GGAGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGACCCAGCATGCTAAGTGTCTAC 180
 Db |||||
 QY 1581 GGAGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGACCCAGCATGCTAAGTGTCTAC 1640
 Db |||||
 QY 181 CCAGGCTGCAAAATACCTA 198
 Db |||||
 QY 1641 CCAGGCTGCAAAATACCTA 1658
 Db |||||

RESULT 7

US-08-800-929A-9
 ; Sequence 9, Application US/08800929A
 ; Patent No. 6133437
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF
 ; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; TITLE OF INVENTION: DISEASE
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Clark & Elbing LLP
 ; STREET: 176 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/800,929A
 ; FILING DATE: 13-FEB-1997

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2691 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-800-929A-9

Query Match 98.4%; Score 194.8; DB 3; Length 2691;
Best Local Similarity 99.0%; Pred. No. 4.7e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAACAGGAGCAGCTT 60
DB 1461 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAACAGGAGCAGCTT 1520
QY 61 GCAAGAGCTCGAATTTATGCTTTTAGGTGAAGGCGATAAAGCTGAAGTGCCTTCCACTGTGGA 120
DB 1521 GCAAGAGCTCGAATTTATGCTTTTAGGTGAAGGCGATAAAGCTGAAGTGCCTTCCACTGTGGA 1580
QY 121 GGAGGGTCCAGGATTCGAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
DB 1581 GGAGGGTCCAGGATTCGAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640
QY 181 CCAGGGTGCATAATACCTA 198
DB 1641 CCAGGGTGCATAATACCTA 1658

RESULT 8
US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-617-053A-9

Query Match 98.4%; Score 194.8; DB 3; Length 2691;
Best Local Similarity 99.0%; Pred. No. 4.7e-60;

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; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-024-433-3

Query Match 87.4%; Score 173; DB 4; Length 1588;
Best Local Similarity 92.4%; Pred. No. 2.6e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
Db |||||
QY 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 885
Db |||||
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 120
Db |||||
QY 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 945
Db |||||
QY 121 GGAGGCTCAGGATTTGGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 180
Db |||||
QY 946 GGAGGCTCAGGATTTGGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 1005
Db |||||
QY 181 CCAGGGTGCATAATACCT 197
Db |||||
QY 1006 CCAGGGTGCATAATACCT 1022
Db |||||

RESULT 11
US-09-016-434-1053
; Sequence 1053, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1053:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: gl016687
US-09-016-434-1053

Query Match 87.4%; Score 173; DB 4; Length 1659;
Best Local Similarity 92.4%; Pred. No. 2.7e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
Db |||||
QY 874 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 933
Db |||||
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 120
Db |||||
QY 934 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 993
Db |||||
QY 121 GGAGGCTCAGGATTTGGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 180
Db |||||
QY 994 GGAGGCTCAGGATTTGGAAGCGGATATAAGTGAAGTCTTCCACTGTGGA 1053
Db |||||
QY 181 CCAGGGTGCATAATACCT 197
Db |||||
QY 1054 CCAGGGTGCATAATACCT 1070
Db |||||

RESULT 12
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 87.4%; Score 173; DB 2; Length 2540;
Best Local Similarity 92.4%; Pred. No. 3.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATATCTAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATATCTAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGCCCTGGACCCATGCTTAAGTGTCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGCCCTGGACCCATGCTTAAGTGTCTAT 1005
QY 181 CCAGGGTGCATAATCT 197
Db 1006 CCAGGGTGCATAATCT 1022
RESULT 13
US-09-392-580-1
Query Match 87.4%; Score 173; DB 3; Length 2540;
Best Local Similarity 92.4%; Pred. No. 3.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
FILE REFERENCE: RTS-0072
CURRENT APPLICATION NUMBER: US/09/392,580
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2540
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..(1527)
US-09-392-580-1
Query Match 87.4%; Score 173; DB 3; Length 2540;
Best Local Similarity 92.4%; Pred. No. 3.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATATCTAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATATCTAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGCCCTGGACCCATGCTTAAGTGTCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGCCCTGGACCCATGCTTAAGTGTCTAT 1005
QY 181 CCAGGGTGCATAATCT 197
Db 1006 CCAGGGTGCATAATCT 1022
RESULT 14
US-09-201-936-3
Query Match 87.4%; Score 173; DB 3; Length 2540;
Best Local Similarity 92.4%; Pred. No. 3.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003

QY 1 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATATCTAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATATCTAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGCCCTGGACCCATGCTTAAGTGTCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGCCCTGGACCCATGCTTAAGTGTCTAT 1005
QY 181 CCAGGGTGCATAATCT 197
Db 1006 CCAGGGTGCATAATCT 1022
RESULT 15
US-09-023-655-900
Query Match 87.4%; Score 173; DB 4; Length 2540;
Best Local Similarity 92.4%; Pred. No. 3.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 900:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1184319
; US-09-023-655-900
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Query Match      87.4%; Score 173; DB 4; Length 2540;
Best Local Similarity 92.4%; Pred.No. 3.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTTAAACAAGGAGCGAGCTT 60
Db 826 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTTAAACAAGGAGCGAGCTT 885

Qy 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945

Qy 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCGAGCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGACCCCTGGGACCGAGCATGCTAAGTGCTAT 1005

Qy 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022
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Search completed: October 22, 2004, 22:14:06
Job time : 55 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 21:14:39 ; Search time 242 Seconds

(without alignments)
4192.299 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgatcggttac.....accagggtgcaataacctta 198

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	198	100.0	2100	9	US-09-201-936-9
2	198	100.0	2100	17	US-10-636-065-224
3	198	100.0	2100	17	US-10-600-272-9
4	194.8	98.4	2691	9	US-09-974-592-9
5	173	87.4	1588	13	US-10-024-433-3
6	173	87.4	1659	16	US-10-305-720-1053
7	173	87.4	2404	9	US-09-964-899-38
8	173	87.4	2540	9	US-09-201-936-3
9	173	87.4	2540	15	US-10-007-926A-274
10	173	87.4	2540	15	US-10-366-307-1
11	173	87.4	2540	15	US-10-388-360-331
12	173	87.4	2540	16	US-10-641-643-900

13	173	87.4	2540	17	US-10-636-065-218
14	173	87.4	2540	17	US-10-600-272-3
15	173	87.4	3000	17	US-10-636-065-231
16	173	87.4	5232	9	US-09-974-592-3
17	149	75.3	1758	16	US-10-343-115-1
18	149	75.3	1758	16	US-10-343-115-3
19	147.4	74.4	1559	13	US-10-024-433-1
20	134.4	67.9	152331	13	US-10-095-407-16
21	109.6	55.4	176373	13	US-10-095-407-17
22	77.8	39.3	302	11	US-09-969-034-2480
23	76	38.4	255	15	US-10-102-524-906
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25	76	38.4	2563	16	US-10-641-643-894
26	76	38.4	2601	15	US-10-232-286-3
27	76	38.4	2676	9	US-09-201-936-5
28	76	38.4	2676	17	US-10-636-065-220
29	76	38.4	2676	17	US-10-600-272-5
30	76	38.4	2916	16	US-10-240-425-1436
31	76	38.4	2916	17	US-10-776-827-11
32	76	38.4	3076	9	US-09-954-456-1635
33	76	38.4	3076	14	US-10-197-290-1
34	76	38.4	3076	15	US-10-388-263-157
35	76	38.4	3076	17	US-10-776-827-11
36	76	38.4	3076	17	US-10-141-618-5
37	76	38.4	3164	15	US-10-269-909-5
38	76	38.4	3165	15	US-10-172-118-564
39	76	38.4	3165	15	US-10-366-307-5
40	76	38.4	3165	16	US-10-342-887-564
41	76	38.4	3165	15	US-10-353-461-7
42	76	38.4	3734	15	US-10-353-461-7
43	76	38.4	5844	10	US-09-971-392-253
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45	76	38.4	6669	9	US-09-974-592-5

ALIGNMENTS

RESULT 1
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 100.0%; Score 198; DB 9; Length 2100;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACGTTAACAAGGACAGCTT 60

Db 916 TATGAGACCGATCGTTACTTTTGGAAACATGGATATACCTCGTTAAACAAGACGAGCTT 975
Qy 61 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
Db 976 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 1035
Qy 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCAAGCATGCTAAAGTGTAC 180
Db 1036 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCAAGCATGCTAAAGTGTAC 1095
Qy 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113

RESULT 2

US-10-636-065-224
; Sequence 224, Application US/10636065

; Publication No. US20040127694A1
; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.

; APPLICANT: LaCasse, Eric

; APPLICANT: Baird, Stephen

; APPLICANT: Holcik, Martin

; APPLICANT: Young, Sean

; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses

; FILE OF INVENTION: Thereof

; FILE REFERENCE: 07891/025005

; CURRENT APPLICATION NUMBER: US/10/636,065

; CURRENT FILING DATE: 2003-08-07

; PRIOR APPLICATION NUMBER: 09/672,717

; PRIOR FILING DATE: 2000-09-28

; NUMBER OF SEQ ID NOS: 231

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 224

; LENGTH: 2100

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-636-065-224

Query Match 100.0%; Score 198; DB 17; Length 2100;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 916 TATGAAGCAGGATCGTTACTTTTGGAAACATGGATATACCTCGTTAAACAAGACGAGCTT 975

Qy 61 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
Db 976 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 1035

Qy 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCAAGCATGCTAAAGTGTAC 180
Db 1036 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCAAGCATGCTAAAGTGTAC 1095

Qy 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113

RESULT 3

US-10-600-272-9

; Sequence 9, Application US/10600272

; Publication No. US20040157232A1

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.

; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen

; APPLICANT: Liston, Peter

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

; TITLE OF INVENTION: PROBES, AND DETECTION METHODS

; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-600-272-9

Query Match 100.0%; Score 198; DB 17; Length 2100;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCGTTACTTTTGGAAACATGGATATACCTCGTTAAACAAGACGAGCTT 60
Db 916 TATGAAGCAGGATCGTTACTTTTGGAAACATGGATATACCTCGTTAAACAAGACGAGCTT 975

Qy 61 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
Db 976 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 1035

Qy 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCAAGCATGCTAAAGTGTAC 180
Db 1036 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGACCAAGCATGCTAAAGTGTAC 1095

Qy 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113

RESULT 4

US-09-974-592-9

; Sequence 9, Application US/09974592

; Patent No. US20020120121A1

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; FILE OF INVENTION: DISEASE

; FILE REFERENCE: 07891/009004

; CURRENT APPLICATION NUMBER: US/09/974,592

; CURRENT FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: US 09/617,053

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/800,929

; PRIOR FILING DATE: 1997-02-13

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 2691

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-974-592-9

Query Match 98.4%; Score 194.8; DB 9; Length 2691;
Best Local Similarity 99.0%; Pred. No. 4.6e-57;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	TATGAAGCAGGATCGTTACTTTTGGGAACATGGATATACTCAGTTAAACAAGGACAGCTT	60
Db	1461	TATGAAGCAGGATCGTTACTTTTGGGAACATGGATATCTCAGTTAAACAAGGACAGCTT	1520
Qy	61	GCAAGAGCTGATTTATGCTTTTAGGTCGAGGCCATAAGTGAAGTGCCTCCACTGTGGA	120
Db	1521	GCAAGAGCTGATTTATGCTTTTAGGTCGAGGCCATAAGTGAAGTGCCTCCACTGTGGA	1580
Qy	121	GGAGGGCTCAGGATTCGGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGCCTAC	180
Db	1581	GGAGGGCTCAGGATTCGGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGCCTAC	1640
Qy	181	CCAGGGTGCAAATACCTA	198
Db	1641	CCAGGGTGCAAATACCTA	1658

```

RESULT 5
US-10-024-433-3
; Sequence 3, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1388
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-024-433-3

```

```

RESULT 6
US-10-305-720-1053
; Sequence 1053, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program

```

```

; SEQ ID NO 1053
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136Al gi1016687
US-10-305-720-1053

Query Match      87.4%; Score 173; DB 16; Length 1659;
Best Local Similarity 92.4%; Pred. No. 1.5e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0

QY      1  TATGAAAGCAGCATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAAGAGCAGCTT 60
Db      874  TATGAAGCACCAGATCTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGAGCAGCTT 933

QY      61  GCAAGAGCTGGATTTTATGCTTTTAGTGCAAGCGGATAAAGTGAAGTGCTTCCACCTGTGGA 120
Db      934  GCAAGAGCTGGATTTTATGCTTTTAGTGAAGTGATAAAGTGAAGTGCTTCCACCTGTGGA 993

QY      121  GGAGGGCTCAGCGATGGTAAGCCCAAGTGAAGACCCCTGGGACCCAGCATGCTAAGTGCTAC 180
Db      994  GGAGGGCTTAAGTGAATGGAGCCCAAGTGAAGACCCCTGGGACCCAGCATGCTAAGTGCTAT 1053

QY      181  CCAGGGTGCRAATACCT 197
Db      1054  CCAGGGTGCRAATATCT 1070

RESULT 7
US-09-964-899-38
; Sequence 38, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-38

```

Query Match	87.4%	Score 173;	DB 9;	Length 2404;
Best Local Similarity	92.4%;	Pred. No. 1.7e-49;		
Matches 182;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;
Qy 1	TATGAACGCGGATCGTTACTTTTGGAAACATGGATATACTCAGTTACACAGGACGACGTT	60		
Db 827	TATGAACGCGGATCTTTACTTTTGGACATGGATATACTCAGTTAAACAGGACGACGTT	886		
Qy 61	GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGCGATAAAGTGAAGTGCCTTCCACTGTGGGA	120		
Db 887	GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTTCCTGTGGGA	946		
Qy 121	GGAGGGCTCAGGATGGGAAGCCCAAGTGAAGACCCCTGGACACAGATGCTAAAGTGTAC	180		
Db 947	GGAGGGCTACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT	1006		
Qy 181	CCAGGGTGCAAATACCT	197		
Db 1007	CCAGGGTGCAAATATCT	1023		

```
RESULT 8
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: variation
; LOCATION: (2540)....(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match      87.4%; Score 173; DB 9; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.8e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTTACTTTTGGACATGGATATCTAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 945

QY 121 GGAGGGCTCACGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAC 180
DB 946 GGAGGGCTTAAGTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAT 1005

QY 181 CCAGGGTGCAAAATACCT 197
DB 1006 CCAGGGTGCAAAATATCT 1022

RESULT 9
US-10-007-926A-274
; Sequence 274, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; FILE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
```

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US-09-201-936-3
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 274
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: baculoviral iap repeat-containing 4 (BIRC4)
; OTHER INFORMATION: gene.
US-10-007-926A-274

Query Match      87.4%; Score 173; DB 15; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.8e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTTACTTTTGGACATGGATATCTAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 945

QY 121 GGAGGGCTCACGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAC 180
DB 946 GGAGGGCTTAAGTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAT 1005

QY 181 CCAGGGTGCAAAATACCT 197
DB 1006 CCAGGGTGCAAAATATCT 1022

RESULT 10
US-10-366-307-1
; Sequence 1, Application US/10366307
; Publication No. US20030224399A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Determining the Prognosis
; FILE OF INVENTION: For Patients with a Prostate Neoplastic Condition
; FILE REFERENCE: P-LJ 5659
; CURRENT APPLICATION NUMBER: US/10/366,307
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 60/356,956
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-366-307-1

Query Match      87.4%; Score 173; DB 15; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.8e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTTACTTTTGGACATGGATATCTAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 945

QY 121 GGAGGGCTCACGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAC 180
DB 946 GGAGGGCTTAAGTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAT 1005

QY 181 CCAGGGTGCAAAATACCT 197
DB 1006 CCAGGGTGCAAAATATCT 1022
```

RESULT 11
 US-10-388-360-331
 ; Sequence 331, Application US/10388360
 ; Publication No. US2003022528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENOMIC HEALTH
 ; APPLICANT: Baker, Joffe B.
 ; APPLICANT: Cronin, Maureen T.
 ; APPLICANT: Kiefer, Michael C.
 ; APPLICANT: Shak, Steve
 ; APPLICANT: Walker, Michael Graham
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
 ; FILE REFERENCE: 39740-0001US
 ; CURRENT APPLICATION NUMBER: US/10/388,360
 ; CURRENT FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: US 60/412,049
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/364,890
 ; PRIOR FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 331
 ; LENGTH: 2540
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-388-360-331

Query Match 87.4%; Score 173; DB 15; Length 2540;
 Best Local Similarity 92.4%; Pred. No. 1.8e-49;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	1	TATGAAGCAGCGATCGTTTACCTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT	60
Db	826	TATGAAGCAGCGATCGTTTACCTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT	885
QY	61	GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA	120
Db	886	GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA	945
QY	121	GGAGGGCTCAGGATGGAAGCCAAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAC	180
Db	946	GGAGGGCTCAGGATGGAAGCCAAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAC	1005
QY	181	CCAGGTGCAATACCT 197	
Db	1006	CCAGGTGCAATATCT 1022	

RESULT 12
 US-10-641-643-900
 ; Sequence 900, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/641,643
 FILING DATE: 14-Aug-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 900:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2540 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: gl184319
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 900 :
 US-10-641-643-900

Query Match 87.4%; Score 173; DB 16; Length 2540;
 Best Local Similarity 92.4%; Pred. No. 1.8e-49;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	1	TATGAAGCAGCGATCGTTTACCTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT	60
Db	826	TATGAAGCAGCGATCGTTTACCTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT	885
QY	61	GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA	120
Db	886	GCAAGAGCTGGATTTATGCTTTAGTGGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA	945
QY	121	GGAGGGCTCAGGATGGAAGCCAAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAC	180
Db	946	GGAGGGCTCAGGATGGAAGCCAAAGTGAAGACCCCTGGGACCATGCTAAAGTGCTAC	1005
QY	181	CCAGGTGCAATACCT 197	
Db	1006	CCAGGTGCAATATCT 1022	

RESULT 13
 US-10-636-065-218
 ; Sequence 218, Application US/10636065
 ; Publication No. US20040127694A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: LaCasse, Eric
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Holcik, Martin
 ; APPLICANT: Young, Sean
 ; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
 ; FILE REFERENCE: 07891/025005
 ; CURRENT APPLICATION NUMBER: US/10/636,065
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: 09/672,717
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 231
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 218
 ; LENGTH: 2540
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(2540)

OTHER INFORMATION: n=a,t,c, or g
US-10-636-065-218

Query Match 87.4%; Score 173; DB 17; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.8e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTGAAGTCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTGAAGTCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATGGAAGCAAGTGAAGCCCTGGACCAAGTGAAGTGAAGTCTTCCACTGTGGA 180
DB 946 GGAGGGCTCAGGATGGAAGCAAGTGAAGCCCTGGACCAAGTGAAGTGAAGTCTTCCACTGTGGA 1005
QY 181 CCAGGGTGCAAAATACCT 197
DB 1006 CCAGGGTGCAAAATATCT 1022

RESULT 14

US-10-600-272-3

Sequence 3, Application US/10600272
Publication No. US20040157232A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

FILE REFERENCE: 07891/003006

CURRENT APPLICATION NUMBER: US/10/600,272

CURRENT FILING DATE: 2003-06-20

PRIOR APPLICATION NUMBER: US 09/011,356

PRIOR FILING DATE: 1998-02-04

PRIOR APPLICATION NUMBER: PCT/IB96/01022

PRIOR FILING DATE: 1996-08-05

PRIOR APPLICATION NUMBER: US 08/576,956

PRIOR FILING DATE: 1995-12-22

PRIOR APPLICATION NUMBER: US 08/511,485

PRIOR FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 2540

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: variation

LOCATION: (2540)...(2540)

OTHER INFORMATION: N may be any nucleotide

US-10-600-272-3

Query Match 87.4%; Score 173; DB 17; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.8e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTGAAGTCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTGAAGTCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATGGAAGCAAGTGAAGCCCTGGACCAAGTGAAGTGAAGTCTTCCACTGTGGA 180
DB 946 GGAGGGCTCAGGATGGAAGCAAGTGAAGCCCTGGACCAAGTGAAGTGAAGTCTTCCACTGTGGA 1005

QY 181 CCAGGGTGCAAAATACCT 197
DB 1006 CCAGGGTGCAAAATATCT 1022
RESULT 15
US-10-636-065-231
Sequence 231, Application US/10636065
Publication No. US20040127694A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: LaCasse, Eric

APPLICANT: Baird, Stephen

APPLICANT: Holcik, Martin

APPLICANT: Young, Sean

TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses

TITLE OF INVENTION: Thereof

FILE REFERENCE: 07891/025005

CURRENT APPLICATION NUMBER: US/10/636,065

CURRENT FILING DATE: 2003-08-07

PRIOR APPLICATION NUMBER: 09/672,717

PRIOR FILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 231

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 231

LENGTH: 3000

TYPE: DNA

ORGANISM: Homo sapiens

US-10-636-065-231

Query Match 87.4%; Score 173; DB 17; Length 3000;

Best Local Similarity 92.4%; Pred. No. 1.9e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB 1482 TATGAAGCAGGATCGTTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 1541
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTGAAGTCTTCCACTGTGGA 120
DB 1542 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATATAAGTGAAGTGAAGTCTTCCACTGTGGA 1601
QY 121 GGAGGGCTCAGGATGGAAGCAAGTGAAGCCCTGGACCAAGTGAAGTGAAGTCTTCCACTGTGGA 180
DB 1602 GGAGGGCTCAGGATGGAAGCAAGTGAAGCCCTGGACCAAGTGAAGTGAAGTCTTCCACTGTGGA 1661
QY 181 CCAGGGTGCAAAATACCT 197
DB 1662 CCAGGGTGCAAAATATCT 1678

Search completed: October 22, 2004, 23:34:24

Job time : 243 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 20:10:53 ; Search time 1727.5 Seconds
(without alignments)
4176.594 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgatcggttac.....accagggtgcaataaccta 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176.8	89.3	773	6	CD350778 UI-M-GIO-
2	168	84.8	628	1	AI573382 mn83e12.x
3	157	79.3	533	7	CN315131 170004179
4	149	75.3	1851	3	BC056914 Homo sapi
5	147.4	74.4	1789	3	BC046168 Homo sapi
6	108	54.5	617	2	BB663325 BB663325
7	103.4	52.2	504	2	BB650856 BB650856
8	100.8	50.9	318	2	BF659610 BF659610
9	98	49.5	334	4	BM220130 BM220130
10	98	49.5	584	5	BQ552032 BQ552032
11	92.2	46.6	1177	4	BM805359 BM805359
12	90.2	45.6	536	1	AU123207 AU123207
13	88.2	44.5	791	6	CF222542 CF222542
14	87	43.9	373	6	BY662508 BY662508
15	85.2	43.0	849	8	BZ242580 BZ242580
16	84.2	42.5	716	1	AV706807 AV706807
17	81.8	41.3	1472	9	AY398945 AY398945
18	81.8	41.3	1494	9	AY398943 AY398943
19	80.4	40.6	721	9	CE100865 CE100865
20	76.2	38.5	663	5	BU658508 BU658508
21	76	38.4	341	2	AW375598 AW375598
22	76	38.4	354	2	AW375594 AW375594
23	76	38.4	402	2	AW846507 AW846507
24	76	38.4	531	2	AW375599 AW375599

25	76	38.4	532	2	AW846425
26	76	38.4	546	2	AW846421
27	76	38.4	571	2	AW375649
28	76	38.4	582	2	AW846337
29	76	38.4	590	2	BE268377
30	76	38.4	621	2	AW375648
31	76	38.4	680	2	AW375625
32	76	38.4	886	5	BQ652590
33	76	38.4	1799	9	AY420753
34	75.2	38.0	269	2	BE506790
35	74.8	37.8	498	1	AJ678724
36	74.4	37.6	997	7	CO646846
37	74.4	37.6	1045	7	CN645252
38	73.4	37.1	887	4	BJ728878
39	72.4	36.6	690	9	CE697566
40	71.2	36.0	275	9	CG545804
41	70.4	35.6	1748	9	AY420754
42	69.2	34.9	567	4	BE961039
43	69	34.8	735	6	CD284353
44	68.4	34.5	420	8	AQ011995
45	68	34.3	323	2	BE847058

ALIGNMENTS

RESULT 1
CD350778
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD350778 773 bp mRNA linear EST 09-JUL-2003
UI-M-GIO-cgh-g-23-0-UI.r1 NIH BMAP_GIO Mus musculus cDNA clone
IMAGE:6853392 5', mRNA sequence.
CD350778
CD350778.1 GI:31142365
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 773)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
source

Seq primer: pYX-5.
Location/Qualifiers
1. .773
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6853392"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP GIO"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail is AGCGAGCAG. This library was created for the University Iowa Brain Anatomy Project (BNAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

```
ORIGIN
Query Match      89.3%; Score 176.8; DB 6; Length 773;
Best Local Similarity 96.3%; Pred. No. 1e-45;
Matches 181; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 11 GGATGCTTACCTTTGGAACTGATATACCTGATTAACAAGGAGGAGCTG 70
Db 1 GGATGCTTACCTTTGGAACTGATATACCTGATTAACAAGGAGGAGCTG 60

Qy 71 GATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGCTCA 130
Db 61 GATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCA 120

Qy 131 CGGATTGGAAGCAAGTGAAGACCCCTGGGACCATGCTAAGTCTACCCAGGCTCA 190
Db 121 CGGATTGGAAGCAAGTGAAGACCCCTGGGACCATGCTAAGTCTACCCAGGCTCA 180

Qy 191 AATACCTA 198
Db 181 AATACCTA 188
```

```
RESULT 2
AI573382/c
LOCUS      AI573382      628 bp      mRNA      linear      EST 16-APR-1999
DEFINITION mn83e12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. i, mRNA sequence.
ACCESSION  AI573382
VERSION     AI573382.1 GI:4536756
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 628)
AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson.R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 440.
```

```
FEATURES
source
1..628
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse Tcell 937311"
/notes="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG
```

```
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'
ORIGIN
Query Match      84.8%; Score 168; DB 1; Length 628;
Best Local Similarity 93.4%; Pred. No. 6.5e-43;
Matches 185; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 1 TATCAAGCAGCGATCGTTACTTTTGGAACTGATATACCTGATTAACAAGGAGCAGCTT 60
Db 604 TATCAAGCAGCGATCGTTACTTTTGGAACTGATATACCTGATTAACAAGGAGCAGCTT 545

Qy 61 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 544 GCAAGAGCT-GATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 486

Qy 121 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGTCTAC 180
Db 485 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGTCTAC 426

Qy 181 CCAGGTGCAATACCTA 198
Db 425 NCAGGTGCAATACCTA 408
```

```
RESULT 3
CN315131
LOCUS      CN315131      533 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION 17000417981828 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN315131
VERSION     CN315131.1 GI:47331545
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 533)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 533 Std Error: 0.00.
```

```
FEATURES
source
1..533
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9."
/clone_lib="GRN_ES"
/notes="Oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
ORIGIN
Query Match      79.3%; Score 157; DB 7; Length 533;
Best Local Similarity 87.3%; Pred. No. 2.2e-39;
Matches 172; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCGTTACTTTTGGAACTGATATACCTGATTAACAAGGAGCAGCTT 60
Db 155 TATGAAGCAGCGATCGTTACTTTTGGATGTGATATATTCAGTTAACAAGGAGCAGCTT 214

Qy 61 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
```


Db 215 TCAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGGCTTTCACTGTGGA 274
 QY 121 GGAGGGCTCAGGATGGAGCCCAAGTGAAGCCCTGGGACCAAGCATCTAAGTCTAC 180
 Db 275 GGGGGCTAACCTGATTTGGAGCCCAAGGAGCCCTTGGGAACAACATGATAATGGCAT 334

QY 181 CCAGGTGCAATACT 197
 Db 335 CCAGGTGTAATACT 351

RESULT 4
 BC056914
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BC056914 1851 bp mRNA linear HTC 25-JUN-2004
 Homo sapiens baculoviral IAP repeat-containing 8, mRNA (cDNA clone
 IMAGE:5742924), with apparent retained intron.

BC056914.1 GI:34784469
 HTC.

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1851)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalilus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1851)
 Strausberg, R.
 Direct Submission
 Submitted (25-AUG-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,
 Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
 Duane Smalilus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 119 Row: h Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 16974127
 This clone has the following problem: retained intron.

FEATURES

source

1..1851
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742924"
 /tissue_type="Brain, adult medulla"
 /clone_lib="NIH_MGC_119"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 75.3%; Score 149; DB 3; Length 1851;
 Best Local Similarity 84.8%; Pred. No. 1.2e-36;
 Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 1 TATGAAGCACCGATCGTTTACTTTTGGAAACATGGATATACTCAGTTTAAACAAGGAGCAGCTT 60
 Db 1062 TATGAAGCCCGCTCATTACTTTTGGACATGGATGTAATCCGTTAAACAAGGAGCAGCTT 1121
 QY 61 GCAGAGCTGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
 Db 1122 GCAAGAGCTGATTTTATGCTTATAGGTCAAGAGGATAAAGTACAGTGTCTTTCCTGTGGA 1181
 QY 121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAAGTGAAGTCTTGGGAACAGCATGCTAAATGGTAT 1241
 Db 1182 GGAGGGCTAGCAACTGGAAGCCCAAGTGAAGTCTTGGGAACAGCATGCTAAATGGTAT 1241
 QY 181 CCAGGGTGCAAAATACCT 197
 Db 1242 CCAGGGTGCAAAATATCT 1258

RESULT 5

BC046168

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC046168 1789 bp mRNA linear HTC 13-FEB-2003
 Homo sapiens, similar to baculoviral IAP repeat-containing 8, clone
 IMAGE:5742590, mRNA.

BC046168.1 GI:28374455

HTC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strausberg, R.

Direct Submission

Submitted (31-JAN-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcgpaxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 107 Row: i Column: 1

This clone was selected for full length sequencing because it

Db 317 AGCAGCTTGCAGAGTTGGATTTAAGCTTTAGTGTGAGGCGATAAAGTCAAGTGTTC 258

Qy 113 ACTGTGAGGAGGCTCAGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCA 164
 |||||
 Db 257 ACTGTGAGGAGGCTCAGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCA 206
 |||||

RESULT 9
 BM220130/c 334 bp mRNA linear EST 07-JUN-2003
 LOCUS
 DEFINITION
 C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA
 Library (Long) Mus musculus cDNA clone NIA:C0935E08 IMAGE:30037975
 3', mRNA sequence.

ACCESSION
 BM220130
 VERSION
 BM220130.2 GI:31478783
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 334)
 Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 Genome Res. 11 (9), 1553-1558 (2001)
 21429098
 11544199
 On Dec 14, 2001 this sequence version replaced gi:17780130.
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: C0935 row: E column: 08
 Seq primer: -21M13 Forward
 High quality sequence stop: 334
 POLYA=Yes.

FEATURES
 source
 1..334
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="niaEST:C0935E08-3"
 /db_xref="taxon:10090"
 /clone="NIA:C0935E08 IMAGE:30037975"
 /sex="Male"
 /tissue_type="Male genital ridge/mesonephros"
 /dev_stage="12.5-dpc"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 12.5-dpc Male Genital
 Ridge/Mesonephros cDNA Library (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded
 cDNAs were synthesized with an Oligo(dT) primer
 [Invitrogen].
 5'-pGACTAGTCTAGATCGCGCGCCCTTTTTTTTTTTT-3' from
 1.8 ug of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to Lone-linker IL-SalI, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.4 kb. The library was constructed

ORIGIN
 by Yulan Piao (NIA)."

Query Match 49.5%; Score 98; DB 4; Length 334;
 Best Local Similarity 95.3%; Pred. No. 2e-20;
 Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 82 TTAGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGTGAGGAGGGCTCACGGATTGGAAG 141
 |||||
 Db 260 TTAGTGAAGCGGATAAAGTGAAGTGTCTTCCTGTGGAGGAGGGCTCACGGATTGGAAG 201
 |||||

Qy 142 CCAAGTGAAGACCCCTGGGACCAGCATGCTAAAGTCTACCCAGGGT 187
 |||||
 Db 200 CCAAGTGAAGACCCCTGGGACAGCATGCGAAGTGGTACCCAGGGT 155
 |||||

RESULT 10
 BQ552032/c 584 bp mRNA linear EST 20-JUN-2002
 LOCUS
 DEFINITION
 H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
 H4013A06 3', mRNA sequence.

ACCESSION
 BQ552032
 VERSION
 BQ552032.1 GI:21452918
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 584)
 VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,
 Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T.,
 Kartgul, G.J., Luo, A.G., Kelsso, J., Hide, W. and Ko, M.S.H.
 Assembly, verification, and initial annotation of NIA 7.4K mouse
 cDNA clone set
 Genome Res. 12 (12), 1999-2003 (2002)
 22354164
 12466305
 Other ESTs: H4013A06-5
 Contact: Yong Qian
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit http://igsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
 Plate: H4013 row: A column: 06
 Seq primer: -21M13 Forward
 High quality sequence stop: 584
 POLYA=Yes.

FEATURES
 source
 1..584
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="niaEST:H4013A06-3"
 /db_xref="taxon:10090"
 /clone="H4013A06"
 /sex="mixed"
 /dev_stage="mixed"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 clone is among a rearranged set of 7,407 clones from more
 than 20 cDNA libraries."

ORIGIN
 Query Match 49.5%; Score 98; DB 5; Length 584;
 Best Local Similarity 95.3%; Pred. No. 2.3e-20;
 Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 82 TTAGTGAAGCGGATAAAGTGAAGTGTCTTCCTGTGGAGGAGGGCTCACGGATTGGAAG 141
 |||||
 Db 260 TTAGTGAAGCGGATAAAGTGAAGTGTCTTCCTGTGGAGGAGGGCTCACGGATTGGAAG 201
 |||||

```

Qy 142 CCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTACCCAGGCT 187
      |||||
Db 200 CCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTACCCAGGCT 155

RESULT 11
BM805359
LOCUS
DEFINITION BMR05359 1177 bp mRNA linear EST 05-MAR-2002
5', mRNA sequence.
AGENCOURT_6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
BM805359
VERSION BM805359.1 GI:19122182
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1177)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12724 row: m column: 06
High quality sequence stop: 409.

FEATURES
source
Location/Qualifiers
1..1177
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5728685"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_libs="NIH MGC 124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV
(destroyed); Site 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN
Query Match 46.6%; Score 92.2; DB 4; Length 1177;
Best Local Similarity 88.5%; Pred. No. 2e-18;
Matches 100; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 85 GGTGAAGCGGTAAGTGAAGTGTTCACCTGTGGAGAGGGCTCAGGATTGAAGCCA 144
      |||||
Db 142 GGTGAAGGTGATAAGTAAGTGTCTTTCACCTGTGGAGAGGGCTAAGTGAAGGCC 201

Qy 145 AGTGAAGACCCCTGGACAGCATGCTAAGTGTACCCAGGTCGCAATACCT 197
      |||||
Db 202 AGTGAGACCCCTGGACACATGCTAATGTTATCCAGGTCGCAATATCT 254

RESULT 12
AUI23207
LOCUS
DEFINITION AUI23207 NT2RM1 Homo sapiens cDNA clone NT2RM1000921 5', mRNA
sequence.
AUI23207
VERSION AUI23207.1 GI:10947923
KEYWORDS EST.

```

```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 536)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y., Ishii, S., Saito, K.,
Nakamura, Y., Nagai, T., Sugano, S., and Isogai, T.
TITLE HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y.,
Ishii, S., Saito, K., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM1000921"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RM1"
/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN
Query Match 45.6%; Score 90.2; DB 1; Length 536;
Best Local Similarity 86.7%; Pred. No. 7.3e-18;
Matches 98; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 85 GGTGAAGCGGTAAGTGAAGTGTTCACCTGTGGAGAGGGCTCAGGATTGAAGCCA 144
      |||||
Db 99 GGTGAAGGTGATAAGTAAGTGTCTTTCACCTGTGGAGAGGGCTAAGTGAAGGCC 158

Qy 145 AGTGAAGACCCCTGGACAGCATGCTAAGTGTACCCAGGTCGCAATACCT 197
      |||||
Db 159 AGTGAANACCCCTGGGAACAACATGCTAAATGTTATCCAGGTCGCAATATCT 211

RESULT 13
CF222542
LOCUS
DEFINITION AGENCOURT_14926978 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
IMAGE:6981334 5', mRNA sequence.
CF222542
VERSION CF222542.1 GI:33423250
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodidae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 791)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

```


Db 173 GCCAAGTGAGACCCCTTGGGAACAGCATGCGAAGTGGTACCAGGGT 219
|||||
RESULT 15
BZ242580 849 bp DNA linear GSS 12-OCT-2002
LOCUS CH230-252D1.TVB CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION CH230-252D1, genomic survey sequence.
ACCESSION BZ242580
VERSION BZ242580.1 GI:23902844
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 849)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL Unpublished (1999)
COMMENT Other GSSs: CH230-252D1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/oreringinformation.htm>). BAC end
page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
Plate: 252 row: D column: 1
Seq primer: T7
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..849
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/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
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/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"
ORIGIN
Query Match 43.0%; Score 85.2; DB 8; Length 849;
Best Local Similarity 96.7%; Pred. No. 3.4e-16;
Matches 87; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATCTACTAGTTAAACAGGAGCGCTT 60
Db 197 TATGACGACGAGUGCTTACTTTTGGAAACATGGCTACTACTAGTTAAACAGGAGCGCTT 256
QY 61 GCACAGAGCTGGATTTTATGCTTTAGGTGAA 90
Db 257 GCACAGAGCTGGATTTTATGCTTTAGGTGAA 286

Search completed: October 22, 2004, 22:12:15
Job time : 1728.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 10:44:01 ; Search time 113.284 Seconds
(without alignments)
208.999 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARTVFTGWTIYSVNKEQL.....KPSDDPDQHAKYPCCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep23Sep04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	496	2	Aaw19584 Mouse apo
2	386	100.0	496	2	Aaw69297 Murine XI
3	386	100.0	496	5	Abg65666 Mouse inh
4	372	96.4	66	7	Abd61828 Mouse inh
5	372	96.4	496	6	Abp72157 Mouse inh
6	366	94.8	66	7	Abd61827 Rat inh
7	366	94.8	66	7	Abd61810 Human inh
8	366	94.8	110	8	Adp90805 Human XIA
9	366	94.8	236	5	Abg32418 X-linked
10	366	94.8	278	5	Aao20511 Protein o
11	366	94.8	497	2	Aaw19581 Human XIA
12	366	94.8	497	2	Aaw69294 Human XIA
13	366	94.8	497	3	Aay59451 Human X-1
14	366	94.8	497	3	Aay99985 Human inh
15	366	94.8	497	5	Abg65663 Human inh
16	366	94.8	497	7	Adb80961 RING-SH c
17	366	94.8	497	7	Adi39804 Human inh
18	366	94.8	497	8	Adh74639 Human XIA
19	366	94.8	497	8	Adl70166 Human X c
20	357	92.5	496	7	Aaw19745 Mouse inh
21	334	86.5	66	7	Abd61820 Human inh
22	334	86.5	236	3	Aay81440 Human TIA
23	334	86.5	236	4	Aae00365 Human IAP
24	334	86.5	236	5	Aau75066 Human tes
25	334	86.5	236	5	Abg32417 Inhibitor

26	334	86.5	464	5	AAU75747 Human Inh
27	328	85.0	66	4	AAE00366 Chimpanze
28	325	84.2	66	7	ADB61831 Gorilla i
29	325	84.2	236	4	AAE00367 Gorilla i
30	306	79.3	57	7	ADB61832 Unidentif
31	279	72.3	53	7	ADI39821 Human NAI
32	279	72.3	66	7	ADB61829 Chicken i
33	260	67.4	151	5	ADK34975 Novel hum
34	258	66.8	52	7	ADB61830 Bovine inh
35	212	54.9	68	7	ADB61833 Zebra fls
36	198	51.3	68	7	ADB61813 Human inh
37	198	51.3	442	8	ADO26592 Human API
38	198	51.3	557	6	ABP72159 Inhibitor
39	198	51.3	604	2	AAW19582 Human apo
40	198	51.3	604	2	AAW19747 Human inh
41	198	51.3	604	2	AAW13546 Human C-I
42	198	51.3	604	2	AAW69295 Human HIA
43	198	51.3	604	2	AAV52703 Human cel
44	198	51.3	604	2	AAV33997 Human cel
45	198	51.3	604	5	ABG65664 Human inh

ALIGNMENTS

RESULT 1

AAW19584
ID AAW19584 standard; protein; 496 AA.

XX AC AAW19584;

XX XX 02-SEP-1997 (first entry)

XX DE Mouse apoptosis inhibitor M-XIAP.

XX KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
KW HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Domain 26..93

FT Domain /label= BIR-1

FT Domain 163..230

FT Domain /label= BIR-2

FT Domain 264..329

FT Domain /label= BIR-3

FT Domain 438..483

FT Domain /label= Ring_zinc_finger

XX WO9706255-A2.

XX PD 20-FEB-1997.

XX XX 05-AUG-1996; 96WO-IB001022.

XX PR 04-AUG-1995; 95US-00511485.

XX PR 22-DEC-1995; 95US-00576956.

XX PA (UYOT-) UNIV OTTAWA.

XX PI Korneluk RG, Mackenzie AE, Baird S, Liston P;

XX DR WPI; 1997-154262/14.

XX DR N-PSDB; AAT70839.

XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.

XX XX Claim 27; Page 79-80; 219pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a zinc
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The M-XIAP amino acid sequence
 CC was deduced from the m-xiap gene (AAT70839) isolated from a mouse embryo
 CC cDNA library. The IAP oligopeptides can be expressed in host cells (in
 CC vitro or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease
 XX Sequence 496 AA;

Query Match 100.0%; Score 386; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.9e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIIVTGTWYISVKNQQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDQHKACY 60
 DB 264 YEARIIVTGTWYISVKNQQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDQHKACY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 2
 AAW69297
 ID AAW69297 standard; protein; 496 AA.
 XX
 AC AAW69297;
 XX
 DT 13-NOV-1998 (first entry)
 XX
 DE Murine XIAP protein.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
 XX
 OS Mus sp.

XX WO9835693-A2.
 XX 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98WO-IB000781.
 XX
 PR 13-FEB-1997; 97US-00800929.
 XX
 PA (UYOT-) UNIV OTTAWA.
 XX
 PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 XX
 DR WPI; 1998-467164/40.
 DR N-PSDB; AAW55041.
 XX

PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
 PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX

PS Disclosure; Fig 4; 147pp; English.

XX This sequence is the murine XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,

CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 XX

SQ Sequence 496 AA;

Query Match 100.0%; Score 386; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.9e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVKNQQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDQHKACY 60
 DB 264 YEARIIVTGTWYISVKNQQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDQHKACY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 3
 ABG65666
 ID ABG65666 standard; protein; 496 AA.
 XX
 AC ABG65666;
 XX

DT 26-AUG-2002 (first entry)
 XX
 DE Mouse inhibitor of apoptosis, XIAP.

XX Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
 KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 KW embryonic development; viral pathogenesis; autoimmune disorder;
 KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 KW herpes virus infection; pox virus infection; adenovirus infection;
 KW proliferative disease.
 XX

OS Mus sp.

XX WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 PA (ABGE-) AEGERA THERAPEUTICS INC.

XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.
 XX N-PSDB; ABK93872.

PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 XX

PS Example 12; Fig 4; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for

CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC protein sequence
 CC
 CC Sequence 496 AA;

Query Match 100.0%; Score 386; DB 5; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.9e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARTVTEGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKSEDPWDQHKCY 60
 DB 264 YEARTVTEGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKSEDPWDQHKCY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 4
 ADB61828
 ID ADB61828 standard; protein; 66 AA.

AC ADB61828;

DT 04-DEC-2003 (first entry)

DE Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.

XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilm's tumour; BIR 3 domain; mouse; murine.

OS Mus sp.

XX WO2003040172-A2.

PN 15-MAY-2003.

PD 12-NOV-2002; 2002WO-CA001738.

PF 09-NOV-2001; 2001US-0332300P.

PR 08-APR-2002; 2002US-0370934P.

XX (AEGE-) AEGERA THERAPEUTICS INC.

PA Boudreault A, Korneluk RG, La Casse E, Liston P;

XX WPI; 2003-513532/48.

XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.

XX Disclosure; Fig 1B; 53pp; English.

XX This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, renal cell carcinoma
 CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
 CC that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC which was used to demonstrate homology to human IAP protein BIR domains
 CC to which the peptides of the invention are targeted to bind.

XX Sequence 66 AA;

Query Match 96.4%; Score 372; DB 7; Length 66;
 Best Local Similarity 97.0%; Pred. No. 1e-38;
 Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARTVTEGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKSEDPWDQHKCY 60

DB 1 YEARTVTEGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKSEDPWDQHKCY 60

QY 61 PGCKYL 66

DB 61 PGCKYL 66

RESULT 5

ABP72157

ID ABP72157 standard; protein; 496 AA.

AC ABP72157;

DT 22-APR-2003 (first entry)

DE Mouse inhibitor of apoptosis protein MIAP3.

XX Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukaemia;
 KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.

OS Mus sp.

XX WO2003004606-A2.

PN 16-JAN-2003.

PD 03-JUL-2002; 2002WO-US021002.

PF 03-JUL-2001; 2001US-00898158.

PR (UYCO) UNIV COLUMBIA NEW YORK.

PA Troy CM, Shelanski ML;

XX WPI; 2003-210351/20.

DR N-PSDB; ABZ58102.

XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 PT treating cancer, neurodegenerative disorder or cardiomyopathy.

PS Disclosure; Fig 15A; 124pp; English.

XX The present sequence is the protein sequence of murine inhibitor of
 CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as

CC an antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,
 CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
 CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and squamous cell carcinoma (all claimed)

XX SQ Sequence 496 AA;

Query Match 96.4%; Score 372; DB 6; Length 496;
 Best Local Similarity 97.0%; Pred. No. 1.1e-37;
 Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 60
 DB 264 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 323

QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 6
 ADB61827
 ID ADB61827 standard; protein; 66 AA.

XX AC ADB61827;

DT 04-DEC-2003 (first entry)

XX DE Rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.

XX KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilms' tumour; BIR 3 domain; rat.

XX OS Rattus sp.

XX PN WO2003040172-A2.

XX XX 15-MAY-2003.

XX PF 12-NOV-2002; 2002WO-CA001738.

XX PR 09-NOV-2001; 2001US-0332300P.

XX PR 08-APR-2002; 2002US-0370934P.

XX XX (AEGE-) AEGERA THERAPEUTICS INC.

XX PI Boudreault A, Korneluk RG, La Casse E, Liston P;

XX DR WPI; 2003-513532/48.

XX XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.

XX PS Disclosure; Fig 1B; 53pp; English.

XX CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat

CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC which was used to demonstrate homology to human IAP protein BIR domains
 CC to which the peptides of the invention are targeted to bind.

XX SQ Sequence 66 AA;

Query Match 94.8%; Score 366; DB 7; Length 66;
 Best Local Similarity 93.9%; Pred. No. 5.8e-38;
 Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 60
 DB 1 YDARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 60

QY 61 PGCKYL 66

DB 61 PGCKYL 66

RESULT 7
 ADB61810
 ID ADB61810 standard; protein; 66 AA.

XX AC ADB61810;

XX DT 04-DEC-2003 (first entry)

XX DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.

XX KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilms' tumour; human; BIR 3 domain.

XX OS Homo sapiens.

XX PN WO2003040172-A2.

XX PD 15-MAY-2003.

XX XX 12-NOV-2002; 2002WO-CA001738.

XX PR 09-NOV-2001; 2001US-0332300P.

XX PR 08-APR-2002; 2002US-0370934P.

XX XX (AEGE-) AEGERA THERAPEUTICS INC.

XX PI Boudreault A, Korneluk RG, La Casse E, Liston P;

XX XX

PA (UYOT-) UNIV OTTAWA.
 XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
 XX WPI; 1997-154262/14.
 DR N-PSDB; AAT70836.
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
 PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
 PT susceptibility to apoptotic disease.
 XX Claim 27; Page 68-70; 219pp; English.
 PS Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a zinc
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
 CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
 CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
 CC or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease
 XX Sequence 497 AA;
 SQ

Query Match 94.8%; Score 366; DB 2; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.1e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIIVTGTWYVNVKQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWQHAKEY 60
 Db 265 YEARIIVTGTWYVNVKQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWQHAKEY 324
 QY 61 PGCKYL 66
 Db 325 PGCKYL 330

RESULT 12
 AAW69294
 ID AAW69294 standard; protein; 497 AA.
 XX AAW69294;
 AC AAW69294;
 XX 13-NOV-1998 (first entry)
 DT Human XIAP protein.
 XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein.
 KW Homo sapiens.
 OS WO9835693-A2.
 XX 20-AUG-1998.
 PD 13-FEB-1998; 98WO-IB000781.
 PF 13-FEB-1997; 97US-00800929.
 XX (UYOT-) UNIV OTTAWA.
 PA Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 XX WPI; 1998-467164/40.
 DR N-PSDB; AAV55038.
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP

PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX Disclosure; Fig 1; 147pp; English.
 XX This sequence is the human XIAP protein, which is an inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis.
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 XX Sequence 497 AA;
 SQ

Query Match 94.8%; Score 366; DB 2; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.1e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIIVTGTWYVNVKQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWQHAKEY 60
 Db 265 YEARIIVTGTWYVNVKQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWQHAKEY 324
 QY 61 PGCKYL 66
 Db 325 PGCKYL 330

RESULT 13
 AAY59451
 ID AAY59451 standard; protein; 497 AA.
 XX AAY59451;
 AC AAY59451;
 XX 24-MAR-2000 (first entry)
 DT Human XIAP protein sequence.
 XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KW transforming growth factor-beta activated kinase 1; monocyte migration;
 KW TAK1 binding protein 1; extracellular matrix protein production;
 KW cell growth inhibitor; beta-amyloid protein deposition;
 KW immunosuppression; Transforming growth factor-beta.
 XX Homo sapiens.
 OS JPL11326328-A.
 XX 26-NOV-1999.
 PD 13-MAY-1998; 98JP-00130378.
 PF 13-MAY-1998; 98JP-00130378.
 PR (MATS/) MATSUMOTO K.
 PA WPI; 2000-078337/07.
 XX N-PSDB; AAZ48862.
 DR Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein.
 XX Claim 3; Page 28-30; 43pp; Japanese.
 XX This sequence represents the human XIAP protein. The invention relates to
 CC a method for screening a substance inhibiting the formation of a complex

CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
 CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
 CC protein 1 (TAB1) and a substance to be tested are contacted with each
 CC other and then the presence or formation of a complex between XIAP and
 CC TAB1 is detected. The substance can be used as a drug for extracellular
 CC matrix protein production enhancement, cell growth inhibition, monocyte
 CC migration, physiologically active substance induction, immunosuppression,
 CC and beta-amyloid protein deposition. A substance inhibiting the formation
 CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
 CC (Transforming growth factor-beta) type I and/or type II receptor is
 CC useful as a drug
 XX
 XX SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.1e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVTGWTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWQHAKEY 60
 DB 265 YEARIFTGWTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWQHAKEY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 14
 AAY99985
 ID AAY99985 standard; protein; 497 AA.
 XX AAY99985;
 XX
 DT 07-NOV-2000 (first entry)
 XX Human X-linked inhibitor of apoptosis.
 DE
 XX X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;
 KW antiinflammatory; cytostatic; tumour.
 XX
 OS Homo sapiens.
 XX
 XX US6087173-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 09-SEP-1999; 99US-00392580.
 XX
 PR 09-SEP-1999; 99US-00392580.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 PI Bennett CF, Cowseert LM, Ackermann EU;
 XX
 DR WPI; 2000-498201/44.
 DR N-PSDB; AAA64901.
 XX
 XX Antisense compound useful for research reagents, diagnostics, prophylaxis
 PT and for treating disorders associated with X-linked inhibitor of
 PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
 XX
 XX Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis (the
 CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
 CC more effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated with
 CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 CC prophylactically to prevent infection, inflammation or tumour formation
 XX

SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.1e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVTGWTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWQHAKEY 60
 DB 265 YEARIFTGWTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWQHAKEY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 15
 ABG65663
 ID ABG65663 standard; protein; 497 AA.

XX AC ABG65663;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 XX Human inhibitor of apoptosis, XIAP.
 XX
 KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
 KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 KW embryonic development; viral pathogenesis; autoimmune disorder;
 KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 KW herpes virus infection; pox virus infection; adenovirus infection;
 KW proliferative disease.

XX OS Homo sapiens.

XX PN WO200226968-A2.

XX PD 04-APR-2002.

XX PF 27-SEP-2001; 2001WO-CA001379.

XX PR 28-SEP-2000; 2000US-00672717.

XX (UYOT-) UNIV OTTAWA.

PA (AECE-) AEGERA THERAPEUTICS INC.

PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.

DR N-PSDB; ABK93869.

XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.

XX Example 12; Fig 1; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP

CC protein sequence
XX
SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 5; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.1e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTGTTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGGLTDWKPSDDPDQHKCY 60
Db 265 YEARIVTGTTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGGLTDWKPSDDPDQHKCY 60
QY 61 PGCKYL 66
Db 325 PGCKYL 330

Search completed: October 22, 2004, 11:16:32
Job time : 116.284 secs

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OM protein - protein search, using sw model

Run on: October 22, 2004, 10:50:26 ; Search time 125,104 Seconds
(without alignments)
303,544 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARIVTFTWTIYSYNKEQL.....KPSDEPDWQHAKYCPGCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_spot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366	94.8	496	1 BIR4 RAT	Q9r0i6 rattus norv
2	366	94.8	496	2 Q9ESF0	Q9esf0 rattus norv
3	366	94.8	497	1 BIR4 HUMAN	P98170 homo sapien
4	366	94.8	501	2 Q9EQ04	Q9eq04 rattus norv
5	361	93.5	501	2 Q9EQ05	Q9eq05 rattus norv
6	357	92.5	496	1 BIR4 MOUSE	Q9eq09 mus musculu
7	334	86.5	236	1 BIR8 HUMAN	Q9ep09 homo sapien
8	334	86.5	236	2 Q6PIA0	Q6pia0 homo sapien
9	334	86.5	236	2 AAH39318	Aah39318 homo sapi
10	334	86.5	338	2 Q6IPV1	Q6ipv1 homo sapien
11	334	86.5	338	2 AAH71665	Aah71665 homo sapi
12	328	85.0	236	1 BIR8_PANTR	Q9sm72 pan troglod
13	325	84.2	236	1 BIR8_GORGO	Q9sm71 gorilla gor
14	306	79.3	106	2 Q9ERW6	Q9erw6 homo sapien
15	279	72.3	493	2 Q8UW78	Q8uw78 gallus gall
16	258	66.8	109	2 Q8WMY4	Q8wmy4 bos taurus
17	212	54.9	322	2 Q6DEB7	Q6deb7 brachydanio
18	212	54.9	405	2 Q8UWH2	Q8uwh2 brachydanio
19	212	54.9	415	2 Q7SXU1	Q7sxu1 brachydanio
20	204	52.8	280	2 Q6VTV9	Q6vtv9 choristoneu
21	204	52.8	280	2 AAQ91688	Aaq91688 choristoneu
22	198	51.3	604	1 BIR3 HUMAN	Q13489 homo sapien
23	196	50.8	287	2 Q6E7G7	Q6e7g7 anticarsia
24	196	50.8	358	1 FIAP_PIG	Oc2640 sus scrofa
25	192	49.7	195	2 Q9IA70	Q9ia70 gallus gall
26	192	49.7	197	2 Q9IA69	Q9ia69 gallus gall
27	192	49.7	602	2 Q9ES99	Q9es99 rattus norv
28	192	49.7	611	1 BIR_CHICK	Q90660 gallus gall
29	190	49.2	268	1 IAP3_NPVP	P41437 orgyia pseu
30	189	49.0	269	2 Q6QXJ6	Q6qxj6 agrotis seg
31	189	49.0	269	2 AAS82685	Aas82685 agrotis s

RESULT 1

ID	BIR4 RAT	STANDARD;	PRT;	496 AA.
AC	Q9R0I6;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)			
DE	(IAP homolog A) (RIAP3) (RIAP-3).			
GN	Name=Birc4; Synonyms=Api3, Xiap;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SAITO N.;			
RT	"Rattus norvegicus X-linked inhibitor of apoptosis (xiap3) mRNA."			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
CC	!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9 (By similarity).			
CC	!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).			
CC	!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains (By similarity).			
CC	!- SIMILARITY: Belongs to the IAP family.			
CC	!- SIMILARITY: Contains 3 BIR repeats.			
CC	!- SIMILARITY: Contains 1 RING-type zinc finger.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AB033366; BAA85304.1; -.			
DR	HSPSP; P98170; 1151.			
DR	InterPro; IPR001370; BIR.			
DR	InterPro; IPR001841; Znf_ring.			
DR	Pfam; PF00653; BIR; 3.			
DR	SMART; SM00238; BIR; 3.			
DR	SMART; SM00184; RING; 1.			
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.			
DR	PROSITE; PS0143; BIR_REPEAT_2; 3.			
DR	PROSITE; PS00518; ZF_RING_1; FALSE_NEG.			
DR	PROSITE; PS00089; ZF_RING_2; 1.			
KW	Apoptosis; Repeat; Zinc-finger.			
FT	REPEAT 26 93 BIR 1.			

32	189	49.0	374	2	Q921N0	Q921n0 mus musculu
33	189	49.0	600	1	BIR3_MOUSE	Q08863 mus musculu
34	189	49.0	616	2	Q804E2	Q804e2 ictalurus p
35	189	49.0	628	2	Q8UWD2	Q8uwd2 brachydanio
36	189	49.0	647	2	Q7T0K2	Q7t0k2 brachydanio
37	189	49.0	654	2	Q6ZM93	Q6zm93 brachydanio
38	189	49.0	654	2	CAE47763	Caе47763 brachydанio
39	185	47.9	346	2	Q8IS31	Q8is31 bombyx mori
40	185	47.9	346	2	Q968T8	Q968t8 bombyx mori
41	185	47.9	589	2	Q9QZC6	Q9qzc6 rattus norv
42	185	47.9	589	2	Q9ESE8	Q9ese8 rattus norv
43	184	47.7	589	2	Q6P6S1	Q6p6s1 rattus norv
44	184	47.7	589	2	AAH62955	Aah62955 rattus no
45	184	47.7	612	1	BIR2_MOUSE	Q62210 mus musculu

ALIGNMENTS

FT	REPEAT	163	230	BIR 2.	
FT	REPEAT	264	329	BIR 3.	
FT	ZN_FING	449	484	RING-type.	
SQ	SEQUENCE	496 AA;	56072 MW;	E250E3C77461A469 CRC64;	
Query Match					
Best Local Similarity 94.8%; Score 366; DB 1; Length 496;					
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;					
Qy	1	YEARIVTFTWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDWQHAKCY	60		
Db	264	YDARIVTFTWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDWQHAKWY	323		
Qy	61	PGCKYL 66			
Db	324	PGCKYL 329			
RESULT 2					
QSF0	QSF0	PRELIMINARY;	PRT;	496 AA.	
AC	Q9BSF0;				
DT	01-MAR-2001 (Tremblrel. 16, Created)				
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)				
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)				
DE	Inhibitor of apoptosis protein 3.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	PubMed=11860601;				
RA	Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;				
RT	"Cloning and characterization of the rat homologues of the Inhibitor				
RT	of Apoptosis protein 1, 2, and 3 genes.";				
RL	BMC Genomics 3:5-5(2002).				
DR	EMBL; AF183429; AAG22969.1; -.				
DR	HSP; P98170; I151.				
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.				
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.				
DR	GO; GO:0008270; F:zinc ion binding; IEA.				
DR	GO; GO:0006516; P:anti-apoptosis; IEA.				
DR	GO; GO:0016567; P:protein ubiquitination; IEA.				
DR	InterPro; IPR001370; BIR.				
DR	InterPro; IPR001841; Znf_ring.				
DR	Pfam; PF00653; BIR; 3.				
DR	SMART; SM00238; BIR; 3.				
DR	SMART; SM00184; RING; 1.				
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.				
DR	PROSITE; PS0143; BIR_REPEAT_2; 3.				
DR	PROSITE; PS50089; ZF_RING_2; 1.				
SQ	SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;				
Query Match					
Best Local Similarity 94.8%; Score 366; DB 2; Length 496;					
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;					
Qy	1	YEARIVTFTWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDWQHAKCY	60		
Db	264	YDARIVTFTWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPDWQHAKWY	323		
Qy	61	PGCKYL 66			
Db	324	PGCKYL 329			
RESULT 3					
BIR4_HUMAN	BIR4_HUMAN	STANDARD;	PRT;	497 AA.	
AC	P98170; Q9N014;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				

DT	01-OCT-2004 (Rel. 45, Last annotation update)				
DE	Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis				
DE	protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)				
DE	(IAP-like protein) (HILP).				
GN	Name=BIRC4; Synonyms=API3, IAP3, XIAP;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=96145249; PubMed=8552191;				
RA	Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,				
RA	Farahani R., McJean M., Ikeda J., Mackenzie A., Korneluk R.G.;				
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related				
RT	family of IAP genes.";				
RL	Nature 379:349-353(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Fetal heart;				
RX	MEDLINE=96256286; PubMed=8654366;				
RA	Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,				
RA	Gifflilan M.C., Shields H., Hardwick J.M., Thompson C.B.;				
RT	"A conserved family of cellular genes related to the baculovirus iap				
RT	gene and encoding apoptosis inhibitors.";				
RL	EMBO J. 15:2685-2694(1996).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Graham D.;				
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Uterus;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,				
RA	Schererch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[5]				
RP	FUNCTION.				
RX	MEDLINE=97373959; PubMed=9230442;				
RA	Deveraux Q.L., Takahashi R., Salvessen G.S., Reed J.C.;				
RT	"X-linked IAP is a direct inhibitor of cell-death proteases.";				
RL	Nature 388:300-304(1997).				
RN	[6]				
RP	MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.				
RX	MEDLINE=21634829; PubMed=11604410; DOI=10.1074/jbc.M109891200;				
RA	Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,				
RA	Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,				
RA	Simpson R.J., Vaux D.L.;				
RT	"HtrA2 promotes cell death through its serine protease activity and				
RT	its ability to antagonize inhibitor of apoptosis proteins.";				
RL	J. Biol. Chem. 277:445-454(2002).				
RN	[7]				
RP	STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.				
RX	MEDLINE=21020961; PubMed=11140637; DOI=10.1038/35050006;				

324 PGCKYL 329

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Db
RESULT 6
BIR4 MOUSE
ID BIR4 MOUSE STANDARD; PRT; 496 AA.
Q60989; Q08865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN Name=Birc4; Synonyms=Api3, Xiap, Aipa, Miha;
DE Mus musculus (Mouse).
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RX Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RL [2]
SEQUENCE FROM N.A.
RP Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -I- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -I- SIMILARITY: Belongs to the IAP family.
CC -I- SIMILARITY: Contains 3 BIR repeats.
CC -I- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
EMBL; U36842; AAC52594.1; -.
DR EMBL; U88990; AAB58376.1; -.
DR HSP: P98170; 1151.
DR MGD; WGI:107572; Birc4.
DR GO; GO:0001719; P:inhibition of caspase activation; IDA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS00143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR KW Apoptosis; Repeat; Zinc-finger.
FT REPEAT 26 93
FT REPEAT 93 BIR 1.
FT REPEAT 163 230
FT REPEAT 264 329 BIR 2.
FT REPEAT 449 484 BIR 3.
FT ZN FING 484 RING-type.
FT CONFLICT 208 208 E -> K (in Ref. 2).
FT CONFLICT 317 317 E -> D (in Ref. 2).
FT FT

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FT CONFLICT 322 322 W -> C (in Ref. 2).
FT CONFLICT 346 346 S -> P (in Ref. 2).
FT CONFLICT 360 360 S -> P (in Ref. 2).
FT CONFLICT 388 388 I -> L (in Ref. 2).
FT CONFLICT 449 449 C -> S (in Ref. 2).
FT CONFLICT 462 462 V -> F (in Ref. 2).
FT CONFLICT 468 468 V -> A (in Ref. 2).
FT CONFLICT 490 490 K -> N (in Ref. 2).
SQ SEQUENCE 496 AA; 56079 MW; EC5FAE0799F2CDD8 CRC64;

Query Match
Best Local Similarity 92.5%; Score 357; DB 1; Length 496;
Matches 62; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIWTFGTWYVNVNKEQLARAGFYALGEGDKVCKFCGGLTDWKPSDPPWQHAKCY 60
Db 264 YEARIWTFGTWYVNVNKEQLARAGFYALGEGDKVCKFCGGLTDWKPSDPPWQHAKWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 7
BIR8_HUMAN
ID BIR8_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN Name=BIRC8; Synonyms=ILP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21481900; PubMed=11597143; DOI=10.1006/geno.2001.6635;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RA "Genomic organization of the X-linked inhibitor of apoptosis and
RT identification of a novel testis-specific transcript.";
RL Genomics 77:181-188(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1128/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Norangel L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX.
CC -!- SUBUNIT: Binds to caspase-9.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- TISSUE SPECIFICITY: Testis specific in normal tissues.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

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DR EMBL; AF420440; AAL30369.1; -.
DR EMBL; AF164682; AAK81892.1; -.
DR HSSP; P98170; IG73.
DR Genew; HGNC:14878; BIRC8.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR REPEAT 1; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
DR PROSITE; PS00518; ZF_RING_1_FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger.
FT REPEAT 7 70 BIR.
FT ZN_FING 189 224 RING-type.
FT CONFLICT 196 196 Y -> H (in Ref. 2).
SQ SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFAD9D CRC64;

Query Match
Best Local Similarity 86.5%; Score 334; DB 1; Length 236;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIWTFGTWYVNVNKEQLARAGFYALGEGDKVCKFCGGLTDWKPSDPPWQHAKCY 60
Db 4 YEARIWTFGTWYVNVNKEQLARAGFYALGEGDKVCKFCGGLTDWKPSDPPWQHAKWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 8
Q6PIA0
ID Q6PIA0 PRELIMINARY; PRT; 236 AA.
AC Q6PIA0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Baculoviral IAP repeat-containing 8.
GN Name=BIRC8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;

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Query Match	86.5%	Score 334;	DB 2;	Length 338;
Best Local Similarity	81.8%;	Pred. No. 2e-31;		
Matches	54;	Conservative 8;	Mismatches 4;	Indels 0;
Gaps	0;			
Qy	1	YEARIIVFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEDPDQHKACY	60	
Db	106	YEALIIIFGTWYISVNKEQLARAGFYALGQEDKVCQCFHCGGGLANWKFKEPDWQHKAWY	165	
Qy	61	PGCKYKL	66	

OS name=arko; synonymms=luPz;
OC Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Vertebrata; Eutelostomi;
Sequence from N.A.
RP
RN [1]
OX NCBI_TaxID=9595;
NCHL TaxID=9595;

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RX MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1128/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -!- SUBUNIT: Binds to caspase-9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC
CC -----
CC EMBL; AY030053; AAK49777.1; -.
CC HSSP; P98170; IG73.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 1.
CC SMART; SM00238; BIR; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
CC PROSITE; PS0143; BIR_REPEAT_2; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC ADAPTOsis; Zinc-finger.
CC REPEAT 7 70
CC ZN FING 189 224 RING-type.
CC SEQUENCE 236 AA; 27120 MW; C3A70E39E442E4C CRC64;
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CC Query Match 84.2%; Score 325; DB 1; Length 236;
CC Best Local Similarity 78.8%; Pred. No. 1.6e-30;
CC Matches 52; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
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CC QY 1 YEARIVTFTWTYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAQCY 60
CC |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC 4 YEAWLITFTWYVSVNKEQLARAGFYALGQEDKIQCFHCGGLANWKPKEDPWEQHAQWY 63
CC
CC QY 61 PGCKYL 66
CC |||:|||||
CC 64 PGCKYL 69
CC
CC Db
CC
CC RESULT 14
CC Q96RW6 PRELIMINARY; PRT; 106 AA.
CC AC Q96RW6;
CC DT 01-DEC-2001 (TrEMBLrel. 19, Created)
CC DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
CC DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CC DE IAP-like protein 3.
CC GN Name=ILP3;
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Mir S.S., Duckett C.S.; to the EMBL/GenBank/DBJ databases.
CC RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC DR EMBL; AF164681; AAK81891.1; -.
CC DR HSSP; P98170; IG3F.
CC GO; GO:0005622; C:intracellular; IEA.
CC
CC Query Match 72.3%; Score 279; DB 2; Length 493;
CC Best Local Similarity 71.2%; Pred. No. 1.1e-24;
CC Matches 47; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
CC
CC QY 1 YEARIVTFTWTYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAQCY 60
CC |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC 264 YERRIQTFLAWIYPVNKEHLAERAGFYSTGNGDHDVCFHCGGLQEWKEDPWDQAKWF 323
CC
CC QY 61 PGCKYL 66
CC |||:|||||
CC 324 PGCKYL 329
CC
CC Db
CC
CC Search completed: October 22, 2004, 11:20:53
CC Job time : 128.104 secs
CC
CC DR GO; GO:0006916; P:anti-apoptosis; IEA.
CC DR InterPro; IPR001370; BIR.
CC DR Pfam; PF00653; BIR; 1.
CC DR SMART; SM00238; BIR; 1.
CC DR PROSITE; PS0143; BIR_REPEAT_2; 1.
CC SQ SEQUENCE 106 AA; 12360 MW; 6EBAD3AEA880A891 CRC64;
CC
CC Query Match 79.3%; Score 306; DB 2; Length 106;
CC Best Local Similarity 91.1%; Pred. No. 1.3e-28;
CC Matches 51; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 11 WIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAQCYGCKYL 66
CC |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC 2 WIYSVNKEQLSRAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHDWKHFGCKYL 57
CC
CC Db
CC
CC RESULT 15
CC Q8UVF8 PRELIMINARY; PRT; 493 AA.
CC AC Q8UVF8;
CC DT 01-MAR-2002 (TrEMBLrel. 20, Created)
CC DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
CC DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CC DE Inhibitor of apoptosis protein 3.
CC GN Name=IAP3;
CC OS Gallus gallus (Chicken).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
CC OC Gallus.
CC OX NCBI_TaxID=9031;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Bridgham J.T., Johnson A.L.;
CC RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC DR EMBL; AF451854; AAL47170.1; -.
CC DR HSSP; P98170; I130.
CC DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
CC DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
CC DR GO; GO:0008270; F:zinc ion binding; IEA.
CC DR GO; GO:0006916; P:anti-apoptosis; IEA.
CC DR GO; GO:0016567; P:protein ubiquitination; IEA.
CC DR InterPro; IPR001370; BIR.
CC DR InterPro; IPR001841; Znf_ring.
CC DR Pfam; PF00653; BIR; 3.
CC DR Pfam; PF00097; Zf-C3HC4; 1.
CC DR SMART; SM00238; BIR; 3.
CC DR SMART; SM00184; RING; 1.
CC DR PROSITE; PS01282; BIR_REPEAT_1; 2.
CC DR PROSITE; PS0143; BIR_REPEAT_2; 3.
CC DR PROSITE; PS00089; ZF_RING_2; 1.
CC DR Metal-binding; Zinc; Zinc-finger.
CC KW SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;
CC SQ
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CDate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
CAccession: S68449
RListon, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, C.

Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: UNIPROT:Q13489; EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184317
C:Function:
A:Description: apoptotic suppressor
C:Keywords: apoptosis; zinc finger
F:553-597/Domain: RING finger homology <RNG>

Query Match 51.3%; Score 198; DB 2; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.8e-14;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIIVTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPMDOHAK 58
Db 255 HAARKPTFFNWPSSVLVNPQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPMVQHAH 314
Qy 59 CYPGCKYL 66
Db 315 WFPRCXYL 322

RESULT 3
JC5964
apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C:Accession: JC5964
R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (iap) fam
A:Reference number: JC5964; MUID:98162622; PMID:9501011
A:Accession: JC5964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: UNIPROT:O62640; GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g2957174
F:307-351/Domain: RING finger homology <RRN>

Query Match 50.8%; Score 196; DB 2; Length 358;
Best Local Similarity 54.4%; Pred. No. 1.9e-14;
Matches 37; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIIVTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPMDOHAK 58
Db 90 YAARKPTFCNWPSSIPVHPQLASAGFYVGHSDVDVKCFCCDGLRCWESGDDPMVQHAH 149
Qy 59 CYPGCKYL 66
Db 150 WFPRCXYL 157

RESULT 4
T10304
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T10304
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10304
A:Status: preliminary; translated from GB/EMBL/DBU
A:Molecule type: DNA
A:Residues: 1-268 <AHR>
A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: UNIPROT:Q13489; EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184317
C:Function:
A:Description: apoptotic suppressor
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match 47.7%; Score 184; DB 2; Length 618;
Best Local Similarity 51.5%; Pred. No. 7e-13;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIIVTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPMDOHAK 58
Db 269 HAARMRTFWPSSVPVQPEQLASAGFYVGNRNDVKCFCCDGLRCWESGDDPMVQHAH 328

Query Match 49.2%; Score 190; DB 2; Length 268;
Best Local Similarity 48.5%; Pred. No. 6.7e-14;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

Qy 3 ARIVTFGTWYSVNK--EQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPMDOHAKCY 60
Db 113 ARLATFAEMPRGLKQRPPELAEGFFYTQGDGKTRCFCCDGLKDWEPDAPWQOHARWY 172
Qy 61 PGCKYL 66
Db 173 DRCEYV 178

RESULT 5
A53989
apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis vir
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53989
R:Binbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polyp
A:Reference number: A53989; MUID:94187094; PMID:8139034
A:Accession: A53989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <BIR>
A:Cross-references: UNIPROT:P41437; GB:L22564; NID:g456111; PIDN:AAB02610.1; PID:g4561114
A:Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as As
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match 49.2%; Score 190; DB 2; Length 268;
Best Local Similarity 48.5%; Pred. No. 6.7e-14;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

Qy 3 ARIVTFGTWYSVNK--EQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPMDOHAKCY 60
Db 113 ARLRTFAEMPRGLKQRPPELAEGFFYTQGDGKTRCFCCDGLKDWEPDAPWQOHARWY 172
Qy 61 PGCKYL 66
Db 173 DRCEYV 178

RESULT 6
S68450
apoptosis inhibitor hiap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-references: UNIPROT:Q13490; EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184317
C:Function:
A:Description: apoptotic suppressor
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match 47.7%; Score 184; DB 2; Length 618;
Best Local Similarity 51.5%; Pred. No. 7e-13;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIIVTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPMDOHAK 58
Db 269 HAARMRTFWPSSVPVQPEQLASAGFYVGNRNDVKCFCCDGLRCWESGDDPMVQHAH 328

QY 59 CYPGCKYL 66
Db 329 WFPKCEFL 336

RESULT 7

JC7568
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7568
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A:Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.
A:Reference number: JC7568; MUID: 21092523; PMID:11162435
A:Contents: Fetal kidney
A:Accession: JC7568
A:Molecule type: mRNA
A:Residues: 1-298 <LIN>
A:Cross-references: UNIPROT:Q96CA5
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, plays a role in the regulation of apoptosis.
C:Genetics:
A:Gene: kiap
A:Map position: 20q13.3
C:Keywords: apoptosis

Query Match 45.9%; Score 177; DB 2; Length 298;
Best Local Similarity 47.8%; Pred. No. 2.1e-12;
Matches 32; Conservative 9; Mismatches 24; Indels 2; Gaps 1;
QY 2 EARIVTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAKE 59
Db 88 ELRLASFVDPLTAEPPELLAAGFFHTGHQDKVKRCFFCYGGLQSWKRGDDPWTEHAKW 147
QY 60 YPGCKYL 66
Db 148 FPKCQFL 154

RESULT 8

A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpgV
C:Species: Cydia pomonella granulosis virus CpgV
C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: A45679
R:Crack, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A:Reference number: A45679; MUID: 93188168; PMID:8445726
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <CRO>
A:Cross-references: UNIPROT:P41436; GB:L05494; NID:G289583; PIDN:AAA43835.1; PID:G289584
A:Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBI:P127015)
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 45.3%; Score 175; DB 2; Length 275;
Best Local Similarity 43.9%; Pred. No. 3.3e-12;
Matches 29; Conservative 13; Mismatches 22; Indels 2; Gaps 1;

QY 3 ARIVTFGTWYVNVK--EQARAGFYALGRGDKVKCFHCGGLTDWKPSDDPDQHAKE 60
Db 110 ARVKSFNWFCMKQRPQEQADAGFFVTGYGDKNTKCFYCDGLKDWEPDVPWEQVRRWF 169
QY 61 PGCKYL 66
Db 170 DRCAVY 175

RESULT 9

S68452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)

A55478

neuronal apoptosis inhibitory protein - human
N:Alternate names: NAIP
C:Species: Homo sapiens (man)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C:Accession: A55478
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; Baird, E.
Cell 80, 167-178, 1995
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in individuals with a form of neurofibromatosis.
A:Reference number: A55478; MUID: 95112344; PMID:7813013
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <ROY>
A:Cross-references: GB:U19251
C:Genetics:
A:Gene: GDB:SMA@; SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein; F470-477/Region: transmembrane #status predicted <TMM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted <TMM2>
F:476/Binding site: ATP (lys) #status predicted
F:618,632,823,923,1035/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 42.6%; Score 164.5; DB 2; Length 1232;
Best Local Similarity 41.2%; Pred. No. 2.1e-10;
Matches 28; Conservative 15; Mismatches 22; Indels 3; Gaps 1;

QY 2 EARIVTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAKE 58
Db 160 EARLASFNWFPYVGISPCVLSAGFVFTGKDTVQCFCGGLGNWEEGDDPWKEHAK 219
QY 59 CYPGCKYL 66
Db 220 WFPKCEFL 227

RESULT 10

T42628
neuronal apoptosis inhibitory protein 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42628
R:Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
Mamm. Genome 10, 761-763, 1999
A:Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for murine neurofibromatosis.
A:Reference number: 222179; MUID: 99315342; PMID:10384056
A:Accession: T42628
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1447 <YAR>
A:Cross-references: UNIPROT:Q9QUK4; EMBL:AF102871; NID:G3860228; PID:G3860229; PIDN:AACT7
C:Genetics:
A:Gene: Naip2

Query Match 41.6%; Score 160.5; DB 2; Length 1447;
Best Local Similarity 41.2%; Pred. No. 7e-10;
Matches 28; Conservative 14; Mismatches 23; Indels 3; Gaps 1;

QY 2 EARIVTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAKE 58
Db 160 EARLESFDPWFYAHGTSFVLSAAGFVFTGKDTVQCFCGGLGNWEEGDDPWKEHAK 219
QY 59 CYPGCKYL 66
Db 220 WFPKCEFL 227

RESULT 11

S68452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)

A: Molecule type: mRNA
A: Residues: 1-36, 'Ar', 37, 'K', 39, 'L', 41-44, 'H', 46-58, 'Q', 60-412, 'A', 414-427, 'A', 429-496
A: Cross-references: EMBL:U45891; NID:G1184313; PDB:1AAC46388.1; FID:G1184314
C: Genetics:
A: Cross-references: FlyBase:FBgn0015247
C: Function:
A: Description: apoptotic suppressor
C: Superfamily: apoptosis inhibitor
C: Keywords: apoptosis; zinc finger
E: 445-489/Domain: RING finger homology <RING>

C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28409
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28409
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <AFO>
A:Cross-references: UNIPROT:Q9YVJ4; EMBL:AF063866; NID:g4049647; PID:g4049647
C:Genetics:

Query Match	32.6%	Score 126;	DB 2;	Length 150;
Best Local Similarity	33.3%;	Pred. No. 6e-07;		
Matches	23;	Conservative 14;	Mismatches 26;	Indels 6; Gaps 2;

QY	2	EARIVTFGTW----	IYSVNKEQLARAGFYALGEGDKVKCFHCGGGGLTDWKPSDDP	WDQHA	57
	:	:	:	:	:
DB	17	QSRINSYENWPISLFFKINR--	LCEAGFFVNTIGDITVCVNCGLKIKWVLYNDP	WIEHS	74
	:	:	:	:	:
QY	58	KCYPGCKYL	66		
DB	75	KWSPNCNYI	83		

Search completed: October 22, 2004, 11:21:44
Job time : 25.1493 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 11:21:03 ; Search time 84.7164 Seconds
(without alignments)
252.231 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARIWFTGWIYSYNKEQL.....KPSDPWDQHKACYPCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US04_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US03_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US02_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US01_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US04_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US03_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US02_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US01_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	386	100.0	66	9 US-09-201-936-24	Sequence 24, Appl
2	386	100.0	66	16 US-10-600-272-24	Sequence 24, Appl
3	386	100.0	496	9 US-09-974-592-10	Sequence 10, Appl
4	386	100.0	496	9 US-09-201-936-10	Sequence 10, Appl
5	386	100.0	496	16 US-10-636-065-225	Sequence 225, Appl
6	386	100.0	496	16 US-10-600-272-10	Sequence 10, Appl
7	366	94.8	66	9 US-09-201-936-25	Sequence 25, Appl
8	366	94.8	66	16 US-10-600-272-25	Sequence 25, Appl
9	366	94.8	107	9 US-09-965-967-20	Sequence 20, Appl
10	366	94.8	236	13 US-10-024-433-4	Sequence 4, Appl
11	366	94.8	278	9 US-09-964-899-39	Sequence 39, Appl
12	366	94.8	497	9 US-09-974-592-4	Sequence 4, Appl
13	366	94.8	497	9 US-09-201-936-4	Sequence 4, Appl

Sequence 2, Appli
Sequence 219, App
Sequence 4, Appli
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Sequence 2, Appli
Sequence 28, Appl
Sequence 29, Appl
Sequence 32, Appl
Sequence 26, Appl
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Sequence 4, Appli
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Sequence 18, Appl
Sequence 28, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 8, Appli
Sequence 2, Appli
Sequence 27, Appl
Sequence 27, Appl
Sequence 14, Appl
Sequence 14, Appl

14 US-10-366-307-2
15 US-10-636-065-219
16 US-10-600-272-4
17 US-10-024-433-2
18 US-10-343-115-2
19 US-10-138-618-28
20 US-10-138-618-28
21 US-10-138-618-29
22 US-10-138-618-32
23 US-09-201-936-26
24 US-10-600-272-26
25 US-09-974-592-6
26 US-09-201-936-6
27 US-10-232-286-4
28 US-10-141-618-6
29 US-10-366-307-6
30 US-10-636-065-221
31 US-10-600-272-6
32 US-10-730-476A-79
33 US-10-353-461-8
34 US-09-201-936-28
35 US-10-041-859-18
36 US-10-600-272-28
37 US-10-041-859-12
38 US-10-323-643-10
39 US-09-974-592-12
40 US-10-041-859-14
41 US-10-041-859-8
42 US-10-041-859-2
43 US-09-201-936-27
44 US-10-600-272-27
45 US-09-974-592-14
US-10-232-286-14

ALIGNMENTS

RESULT 1

; Sequence 24, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN JAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match 100.0%; Score 386; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 9.3e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIWFTGWIYSYNKEQLARGFALGEGDKVCFHCGGJTDWKPSPDWDQHKACY 60
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Db 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-10-600-272-24
; Sequence 24, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-600-272-24

Query Match 100.0%; Score 386; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 9.3e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 60
Db 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 60
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Db 61 PGCKYL 66

RESULT 3
US-09-974-592-10
; Sequence 10, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-10

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Best Local Similarity 100.0%; Pred. No. 7.9e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 60
Db 264 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 5
US-10-636-065-225
; Sequence 225, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
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; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-10

Query Match 100.0%; Score 386; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 7.9e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 60
Db 264 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4
US-09-201-936-10
; Sequence 10, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-10

Query Match 100.0%; Score 386; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 7.9e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 60
Db 264 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKEY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 5
US-10-636-065-225
; Sequence 225, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
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Dh      1 YEARTETFTWIYSVNKEQLARAGFVALGEGDKVKCFHGGGLTDWKPSDDPWEHAKWY 60
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Qy 61 PGCKYL 66
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pb 61 PGCKYL 66

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RESULT 9
US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-965-967-20

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RESULT 10
US-10-024-433-4
; Sequence 4, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-4

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Qy 61 PGCKYL 66
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Db 64 PGCKYL 69

RESULT 11
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US20020174446A1

RESULT 12
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match	94.8%	Score 366;	DB 9;	Length 497;
Best Local Similarity	95.5%	Pred. No. 2.3e-36;		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 11:08:12 ; Search time 28.0746 Seconds
(without alignments)
155.905 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARIIVFTGWIYSVKNQQL.....KPSDPPDQHKACYPGCKVL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	66	2	US-08-511-485-24
2	386	100.0	66	4	US-09-201-936-24
3	386	100.0	66	4	US-09-011-356-24
4	386	100.0	66	4	US-09-201-932-24
5	386	100.0	496	3	US-08-511-485-10
6	386	100.0	496	3	US-09-212-971-10
7	386	100.0	496	3	US-08-800-929A-10
8	386	100.0	496	3	US-09-617-053A-10
9	386	100.0	496	4	US-09-201-936-10
10	386	100.0	496	4	US-09-011-356-10
11	386	100.0	496	4	US-09-672-717-225
12	386	100.0	496	4	US-09-201-932-10
13	366	94.8	66	2	US-08-511-485-25
14	366	94.8	66	4	US-09-201-936-25
15	366	94.8	66	4	US-09-011-356-25
16	366	94.8	66	4	US-09-201-932-25
17	366	94.8	236	3	US-09-239-867-4
18	366	94.8	236	4	US-10-024-433-4
19	366	94.8	497	2	US-08-511-485-4
20	366	94.8	497	3	US-09-212-971-4
21	366	94.8	497	3	US-08-800-929A-4
22	366	94.8	497	3	US-09-617-053A-4
23	366	94.8	497	4	US-08-657-759-2
24	366	94.8	497	4	US-09-201-936-4
25	366	94.8	497	4	US-09-011-356-4
26	366	94.8	497	4	US-09-672-717-219
27	366	94.8	497	4	US-09-201-932-4

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28 334 86.5 236 3 US-09-121-979-4 Sequence 4, Appli
29 334 86.5 236 3 US-09-332-319-4 Sequence 4, Appli
30 334 86.5 236 3 US-09-239-867-2 Sequence 2, Appli
31 334 86.5 236 4 US-10-024-433-2 Sequence 2, Appli
32 279 72.3 53 4 US-08-657-759-19 Sequence 19, Appli
33 233 60.4 50 3 US-08-975-080-28 Sequence 28, Appli
34 233 60.4 50 3 US-08-975-080-28 Sequence 29, Appli
35 233 60.4 50 3 US-08-975-080-32 Sequence 32, Appli
36 198 51.3 68 4 US-08-511-485-26 Sequence 26, Appli
37 198 51.3 68 4 US-09-201-936-26 Sequence 26, Appli
38 198 51.3 68 4 US-09-011-356-26 Sequence 26, Appli
39 198 51.3 68 4 US-09-201-932-26 Sequence 26, Appli
40 198 51.3 442 4 US-09-579-692B-58 Sequence 58, Appli
41 198 51.3 604 2 US-08-511-485-6 Sequence 6, Appli
42 198 51.3 604 3 US-09-212-971-6 Sequence 6, Appli
43 198 51.3 604 3 US-08-800-929A-6 Sequence 4, Appli
44 198 51.3 604 3 US-08-569-749-4 Sequence 6, Appli
45 198 51.3 604 3 US-09-617-053A-6 Sequence 6, Appli

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ALIGNMENTS

RESULT 1

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US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-24

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Query Match 100.0%; Score 386; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVFTGWIYSVKNQQLARAGFALGEGDKVKCFHCGGLTDWKPSDPPDQHKACV 60
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Db 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAACY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAACY 60
Db 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAACY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3
US-09-011-356-24
; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAACY 60
Db 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAACY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 4
US-09-201-932-24
; Sequence 24, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-932-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAACY 60
Db 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAACY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 5
US-08-511-485-10
; Sequence 10, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
```



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/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/511,485
/ FILING DATE: 04-AUG-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 07540/002001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 496 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: both
/ MOLECULE TYPE: protein
/ US-08-511-485-10
/
/ Query Match 100.0%; Score 386; DB 2; Length 496;
/ Best Local Similarity 100.0%; Pred. No. 4.4e-42;
/ Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 YEARIVTGTWIYSVNKQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHKCY 60
/ Db 264 YEARIVTGTWIYSVNKQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHKCY 323
/
/ QY 61 PGCKYL 66
/ Db 324 PGCKYL 329
/
/ RESULT 6
/ US-09-212-971-10
/ Sequence 10, Application US/09212971B
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G
/ APPLICANT: Mackenzie, Alexander E
/ APPLICANT: Liston, Peter
/ APPLICANT: Baird, Stephen
/ APPLICANT: Tsang, Benjamin K
/ APPLICANT: Pratt, Christine
/ TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
/ TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
/ TITLE OF INVENTION: DISEASE
/ FILE REFERENCE: 07891/009002
/ CURRENT APPLICATION NUMBER: US/09/212,971B
/ CURRENT FILING DATE: 1998-12-16
/ EARLIER APPLICATION NUMBER: 60/017,354
/ EARLIER FILING DATE: 1996-04-26
/ EARLIER APPLICATION NUMBER: 60/030,590
/ EARLIER FILING DATE: 1996-11-14
/ EARLIER APPLICATION NUMBER: 08/800,929
/ EARLIER FILING DATE: 1997-02-13
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 496
/ TYPE: PRT
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/ ORGANISM: Mus musculus
/ US-09-212-971-10
/
/ Query Match 100.0%; Score 386; DB 3; Length 496;
/ Best Local Similarity 100.0%; Pred. No. 4.4e-42;
/ Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ QY 1 YEARIVTGTWIYSVNKQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHKCY 60
/ Db 264 YEARIVTGTWIYSVNKQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHKCY 323
/
/ QY 61 PGCKYL 66
/ Db 324 PGCKYL 329
/
/ RESULT 7
/ US-08-800-929A-10
/ Sequence 10, Application US/08800929A
/ Patent No. 6133437
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G
/ APPLICANT: Mackenzie, Alexander E
/ APPLICANT: Liston, Peter
/ APPLICANT: Baird, Stephen
/ APPLICANT: Tsang, Benjamin K
/ APPLICANT: Pratt, Christine
/ TITLE OF INVENTION: DETECTION AND MODULATION OF
/ TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
/ TITLE OF INVENTION: DISEASE
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Clark & Elbing LLP
/ STREET: 176 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/800,929A
/ FILING DATE: 13-FEB-1997
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/030,590
/ FILING DATE: 14-NOV-1996
/ APPLICATION NUMBER: 60/017,354
/ FILING DATE: 26-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bieker-Brady, Kristina
/ REGISTRATION NUMBER:
/ REFERENCE/DOCKET NUMBER: 07891/009001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-428-0200
/ TELEFAX: 617-428-7045
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 496 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-800-929A-10
/
/ Query Match 100.0%; Score 386; DB 3; Length 496;
/ Best Local Similarity 100.0%; Pred. No. 4.4e-42;
/ Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	YEARIVTFTWTWYVYNKEQLARAGFVALGEGDKVKCFHCGGGLTDWKPSDDPWDQHAKCY	60
Db	264	YEARIVTFTWTWYVYNKEQLARAGFVALGEGDKVKCFHCGGGLTDWKPSDDPWDQHAKCY	323

RESULT 8
US-09-617-053A-10
; Sequence 10, Application US/09617053A
; Patent NO. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIJ FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-617-053A-10

Query Match	100.0%;	Score 386;	DB 3;	Length 496;
Best Local Similarity	100.0%;	Pred. No. 4.4e-4;		
Matches 66;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	YEARIVTGTWITYSNKQELARAGFYALGEGDKVKCFHGGGLTDWKPSDPWDQAKY	60	
Db	264	YEARIVTGTWITYSNKQELARAGFYALGEGDKVKCFHGGGLTDWKPSDPWDQAKY	323	
Qy	61	PGCKYL	66	
Db	324	PGCKYL	329	

RESULT 9
US-09-201-936-10
; Sequence 10, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 10
;
; LENGTH: 496
;
; TYPE: CDS
;
; ORGANISM: Mus musculus
US-09-201-916-10

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RESULT 10
US-09-011-356-10
; Sequence 10, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011.356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-10

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RESULT 11
US-09-672-717-225
; Sequence 225, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07B91/025001

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; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-672-717-225

Query Match
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Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 264 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPMDOHAKCY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 12
US-09-201-932-10
; Sequence 10, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-932-10

Query Match
Best Local Similarity 100.0%; Score 386; DB 4; Length 496;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPMDOHAKCY 60
Db 264 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPMDOHAKCY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 13
US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 591912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
```

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; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-25

Query Match
Best Local Similarity 94.8%; Score 366; DB 2; Length 66;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPMDOHAKCY 60
Db 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPMDOHAKCY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 14
US-09-201-936-25
; Sequence 25, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match      94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred.No.1.6e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGCTWIYSVNKQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQHKCY 60
Db 1 YEARIFTGCTWIYSVNKQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQHKCY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 15
US-09-011-356-25
; Sequence 25, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-25

Query Match      94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred.No.1.6e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGCTWIYSVNKQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQHKCY 60
Db 1 YEARIFTGCTWIYSVNKQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQHKCY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

Search completed: October 22, 2004, 11:22:46
Job time : 29.0746 secs
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Title: GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2004, 10:44:01 ; Search time 116.716 Seconds
(without alignments)
208.999 Million cell updates/sec

Title: US-09-654-743-27

Perfect score: 402

Sequence: 1 HAARMRTMYWPSVVFQPE.....ESGDDPWVHAKWFCRCEPL 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	618	2 AAW19583	Aaw19583 Human apo
2	402	100.0	618	2 AAW69296	Aaw69296 Human HIA
3	402	100.0	618	5 ABG65665	Abg65665 Human inh
4	393	97.8	68	7 ADB61816	Adb61816 Human inh
5	393	97.8	438	2 AAW04583	Aaw04583 Human inh
6	393	97.8	459	6 ABP72158	Abp72158 Inhibitor
7	393	97.8	618	2 AAW19746	Aaw19746 Human inh
8	393	97.8	618	2 AAW13545	Aaw13545 Human c-I
9	393	97.8	618	2 AAY33998	Aay33998 Human cel
10	393	97.8	618	6 ABP72160	Abp72160 Human inh
11	393	97.8	618	7 ADB80949	Adb80949 RING-SH c
12	393	97.8	618	7 ABR84600	Abp72158 Inhibitor
13	393	97.8	618	7 ADD25639	Adb80949 RING-SH c
14	393	97.8	618	7 ADG10748	Adg10748 Human STA
15	393	97.8	618	7 ADP65159	Adp65159 Human bac
16	393	97.8	618	8 ADH74641	Adh74641 Human cia
17	393	97.8	618	8 ADL14084	Adl14084 Human sar
18	366	91.0	612	2 AAW13555	Aaw13555 Murine c-
19	366	91.0	612	2 AAW69299	Aaw69299 Murine HI
20	366	91.0	612	6 ABP72156	Abp72156 Mouse inh
21	360	89.6	591	2 AAW19586	Aaw19586 Mouse apo
22	360	89.6	591	5 ABG65668	Abg65668 Mouse inh
23	340	84.6	68	7 ADB61813	Adb61813 Human inh
24	340	84.6	442	8 ADO26592	Ado26592 Human API
25	340	84.6	557	6 ABP72159	Abp72159 Inhibitor

26	340	84.6	604	2 AAW19582	Aaw19582 Human apo
27	340	84.6	604	2 AAW19747	Aaw19747 Human inh
28	340	84.6	604	2 AAW13546	Aaw13546 Human c-I
29	340	84.6	604	2 AAW69295	Aaw69295 Human HIA
30	340	84.6	604	2 AAY52703	Aay52703 Human cel
31	340	84.6	604	2 AAY33997	Aay33997 Human cel
32	340	84.6	604	5 ABG65664	Abg65664 Human inh
33	340	84.6	604	6 ABU07431	Abu07431 Protein d
34	340	84.6	604	6 ABB82739	Abb82739 Human CIA
35	340	84.6	604	7 ADB80948	Adb80948 RING-SH c
36	340	84.6	604	7 AAE39811	Aae39811 Human cel
37	340	84.6	604	8 ADG87135	Adg87135 Human cia
38	340	84.6	604	8 ADH74643	Adh74643 Human cys
39	340	84.6	1140	5 AAU97837	Aau97837 Human CIA
40	340	84.6	1140	7 ADL93367	Adl93367 Human API
41	340	84.6	1140	8 ADO26542	Ado26542 Human API
42	340	84.6	1141	4 AAB50694	Aab50694 Human API
43	324	80.6	600	2 AAW69298	Aaw69298 Murine HI
44	324	80.6	600	6 ABF72155	Abf72155 Mouse inh
45	318	79.1	602	5 ABG65667	Abg65667 Mouse inh

ALIGNMENTS

RESULT 1

AAW19583
ID AAW19583 standard; protein; 618 AA.

XX AAW19583;

DT 02-SEP-1997 (first entry)

XX Human apoptosis inhibitor HIAP-2.

KW Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;

KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;

KW reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 46..113

FT Domain /label= BIR-1

FT Domain 184..250

FT Domain /label= BIR-2

FT Domain 269..336

FT Domain /label= BIR-3

FT Domain 560..605

FT Domain /label= Ring_zinc_finger

WO9706255-A2.

20-FEB-1997.

05-AUG-1996; 96WO-IB001022.

04-AUG-1995; 95US-00511485.

22-DEC-1995; 95US-00576956.

(UYOT-) UNIV OTTAWA.

Korneluk RG, Mackenzie AE, Baird S, Liston P;

WPI; 1997-154262/14.

N-PSDB; AAT70838.

PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease.

PS Claim 27; Page 75-77; 219pp; English.

CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a ring
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The HIAP amino acid sequences
 CC were deduced from cDNA clones (AAW70837 and AAW70838) from a human liver
 CC library. IAP polypeptides can be expressed in host cells (in vitro or in
 CC vivo) and used in methods for treating diseases and disorders involving
 CC apoptosis, esp. in a human diagnosed as HIV-positive or as having AIDS, a
 CC neurodegenerative disease, a myelodysplastic syndrome or an ischaemic
 CC injury selected from myocardial infarction, stroke, reperfusion injury,
 CC or a toxin-induced liver disease

XX Sequence 618 AA;
 SQ
 Query Match 100.0%; Score 402; DB 2; Length 618;
 Best Local Similarity 100.0%; Pred. No. 9.2e-39;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVVPVPEQLASAGFYVYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 60
 DB 269 HAARMRTMYWPSVVPVPEQLASAGFYVYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 328

QY 61 WFPCEFL 68
 DB 329 WFPCEFL 336

RESULT 2

AAW69296
 ID AAW69296 standard; protein; 618 AA.

XX AC AAW69296;

XX AC AAW69296;

DT 13-NOV-1998 (first entry)

XX Human HIAP-2 protein.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.

XX Homo sapiens.

XX WO9835693-A2.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-IB000781.

XX 13-FEB-1997; 97US-00800929.

XX (UYOT-) UNIV OTTAWA.

XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;

XX WPI; 1998-467164/40.

XX N-PSDB; AAV55040.

XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
 PT and NAIP, specifically applied to cancers involving p53 mutations.

XX Disclosure; Fig 3; 147pp; English.

XX This sequence is the human HIAP-2 protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity

CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors

XX Sequence 618 AA;

Query Match 100.0%; Score 402; DB 2; Length 618;
 Best Local Similarity 100.0%; Pred. No. 9.2e-39;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVVPVPEQLASAGFYVYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 60
 DB 269 HAARMRTMYWPSVVPVPEQLASAGFYVYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 328

QY 61 WFPCEFL 68
 DB 329 WFPCEFL 336

RESULT 3

ABG65665

ID ABG65665 standard; protein; 618 AA.

XX AC ABG65665;

XX 26-AUG-2002 (first entry)

XX Human inhibitor of apoptosis, HIAP2.

XX Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
 KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 KW embryonic development; viral pathogenesis; autoimmune disorder;
 KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 KW herpes virus infection; pox virus infection; adenovirus infection;
 KW proliferative disease.

XX Homo sapiens.

XX WO200226968-A2.

XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-CA001379.

XX 28-SEP-2000; 2000US-00672717.

XX (UYOT-) UNIV OTTAWA.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.

XX N-PSDB; ABK93871.

XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.

XX Disclosure; Fig 3; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.

CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC protein sequence
 XX
 SQ Sequence 618 AA;
 Query Match 100.0%; Score 402; DB 5; Length 618;
 Best Local Similarity 100.0%; Pred. No. 9.2e-39;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HAARMRTFMYWSSVPVQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVEHAK 60
 DB 269 HAARMRTFMYWSSVPVQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVEHAK 328
 QY 61 WPPRCFEL 68
 DB 329 WPPRCFEL 336
 RESULT 4
 ID ADB61816 standard; protein; 68 AA.
 AC ADB61816;
 DT 04-DEC-2003 (first entry)
 XX Human inhibitor of apoptosis (IAP) protein HIAP2 BIR3 domain.
 DE baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilms' tumour; human; BIR 3 domain.
 XX Homo sapiens.
 OS
 XX WO2003040172-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 12-NOV-2002; 2002WO-CA001738.
 PF
 XX 09-NOV-2001; 2001US-0323300P.
 PR
 XX 08-APR-2002; 2002US-0370934P.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX Boudreault A, Korneluk RG, La Casse E, Liston P;
 PI
 XX WPI; 2003-513532/48.
 DR
 XX Polypeptide capable of forming a complex with a polypeptide comprising a
 FT baculovirus inhibitor of apoptosis repeat domain useful for treating a
 PT cancer and other neoplasms.
 PT
 XX Disclosure; Fig 1A; 53pp; English.
 PS
 XX This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders

CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein HIAP2 BIR3 domain
 CC against which the peptides of the invention are targeted to bind.

XX Sequence 68 AA;
 SQ

Query Match 97.8%; Score 393; DB 7; Length 68;
 Best Local Similarity 98.5%; Pred. No. 8.9e-39;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTFMYWSSVPVQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVEHAK 60
 DB 1 HAARMRTFMYWSSVPVQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVEHAK 60
 QY 61 WPPRCFEL 68
 DB 61 WPPRCFEL 68

RESULT 5
 AAW04583
 ID AAW04583 standard; protein; 438 AA.
 XX
 AC AAW04583;
 DT 07-FEB-1997 (first entry)
 XX Human inhibitor of apoptosis gene 1.
 DE
 XX Inhibitor of apoptosis 1; hIAP-1; degenerative disease;
 KW rheumatoid arthritis; septic shock; antiviral; trauma; stroke;
 KW cell death; oncogenesis; cancer; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO9635703-A1.
 PN
 XX 14-NOV-1996.
 PD
 XX 11-MAY-1995; 95WO-US005922.
 PF
 XX 11-MAY-1995; 95WO-US005922.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX He WW, Hudson PL, Rosen CA;
 PI
 XX WPI; 1996-518608/51.
 DR
 XX N-PSDB; AAT43709.
 XX
 XX Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful for
 PT treating degenerative diseases, as antiviral defence mechanism and
 PT preventing cell death during trauma and strokes.
 PT
 XX Claim 1; Page 40-41; 53pp; English.
 PS
 XX Human inhibitor of apoptosis 1 (hIAP-1) (AAW04583) is a protein useful
 CC for treating degenerative diseases, rheumatoid arthritis, septic shock,

CC as an antiviral defence mechanism, and for preventing cell death during
 CC strokes or trauma. Its amino acid sequence was deduced from a cDNA clone
 CC (AA743709) that can be obtd. from human Jurkat cell lines or human
 CC osteoclastoma stromal cell lines. Recombinant hIAP-1 can be produced in
 CC prokaryotic or eukaryotic host cells, or expressed in vivo. It can also
 CC be used to screen for modulators of hIAP-1 activity

XX SQ Sequence 438 AA;

Query Match 97.8%; Score 393; DB 2; Length 438;
 Best Local Similarity 98.5%; Pred. No. 7.3e-38;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAAMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
 |||||
 DB 89 HAAMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 148
 |||||

QY 61 WPRCEFL 68
 |||||

DB 149 WPRCEFL 156
 |||||

RESULT 6
 ABP72158
 ID ABP72158 standard; protein; 459 AA.

XX AC ABP72158;

XX DT 22-APR-2003 (first entry)

XX DE Inhibitor of apoptosis protein CIAP1.

XX KW Inhibitor of apoptosis; CIAP1; apoptosis; cancer; leukaemia; lymphoma;
 XX neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.

XX OS Unidentified.

XX PN WO2003004606-A2.

XX PD 16-JAN-2003.

XX PF 03-JUL-2002; 2002WO-US021002.

XX PR 03-JUL-2001; 2001US-00898158.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Troy CM, Shelanski ML;

XX DR WPI; 2003-210351/20.

XX DR N-PSDB; ABZ58103.

XX PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 XX treating cancer, neurodegenerative disorder or cardiomyopathy.

XX PS Disclosure; Fig 16a; 124pp; English.

XX The present sequence is the protein sequence of inhibitor of apoptosis
 CC protein CIAP1. The invention provides a nucleic acid, such as an
 CC antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,
 CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
 CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and squamous cell carcinoma (all claimed)

XX SQ Sequence 459 AA;

Query Match 97.8%; Score 393; DB 6; Length 459;

Best Local Similarity 98.5%; Pred. No. 7.7e-38;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAAMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
 |||||
 DB 269 HAAMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 328
 |||||

QY 61 WPRCEFL 68
 |||||

DB 329 WPRCEFL 336
 |||||

RESULT 7

AAW19746

ID AAW19746 standard; protein; 618 AA.

XX AC AAW19746;

XX DT 16-SEP-1997 (first entry)

XX DE Human inhibitor of apoptosis protein homologue MIHB.

XX KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;
 XX degenerative disease; infectious disease; autoimmune disease; cancer;
 XX therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 46..113

XX FT /label= BIR

XX FT Region 184..250

XX FT /label= BIR

XX FT Region 269..337

XX FT /label= BIR

XX FT Region 569..606

XX FT /label= RING_finger

XX PN WO9723501-A1.

XX PD 03-JUL-1997.

XX PF 20-DEC-1996; 96WO-AU0000827.

XX PR 22-DEC-1995; 95AU-00007275.

XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX PI Vaux DL;

XX DR WPI; 1997-350966/32.

XX DR N-PSDB; AAT72711.

XX PT Isolated protein homologues of viral inhibitors of apoptosis - used to
 XX modulate apoptosis for treatment of degenerative, infectious or
 XX auto-immune diseases and cancer.

XX PS Claim 8; Page 51-54; 136pp; English.

XX Mammalian IAP homologue B (MIHB) (AAW19746) is a human homologue of
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid sequence
 CC was deduced from a cDNA clone (see also AAT72711) isolated from a human
 CC foetal liver cDNA library using primers based on human EST sequences that
 CC resembled the BIR repeats of Orygia pseudotsuguta polyhedrosis virus IAP.
 CC IAP homologues (see also AAW19745 and AAW19745-52) and their derivatives
 CC and chemical analogues can be used in methods for modulating apoptosis in
 CC animal cells, specifically for treatment, by inhibition, of degenerative
 CC and infectious disease or, by promotion, of cancer and autoimmune disease

XX SQ Sequence 618 AA;

Query Match 97.8%; Score 393; DB 2; Length 618;

Best Local Similarity 98.5%; Pred. No. 1.1e-37;

Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 60
 |||||
 Db 269 HAARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 328
 |||||
 QY 61 WPRCEFL 68
 |||||
 Db 329 WPRCEFL 336

RESULT 8
 AAW13545
 ID AAW13545 standard; protein; 618 AA.
 XX
 AC AAW13545;
 DT 22-JUL-1997 (first entry)
 XX
 DE Human c-IAP1.
 KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
 KW myocardial infarction; nephritis; HIV.
 XX
 OS Homo sapiens.
 XX
 PN WO9706182-A1.
 XX
 PD 20-FEB-1997.
 XX
 PF 06-AUG-1996; 96WO-US012860.
 XX
 PR 08-AUG-1995; 95US-00512946.
 PR 08-DEC-1995; 95US-00569749.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Rothe M, Goeddel DV;
 XX
 DR WPI; 1997-154209/14.
 DR N-PSDB; AAT61590.
 XX
 PT Nucleic acids encoding cellular inhibitor of apoptosis proteins - useful
 PT for apoptosis regulation in cells to reduce or increase apoptosis and for
 PT pharmacological screening.
 XX
 PS Disclosure; Page 18-20; 35pp; English.
 XX
 CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
 CC AAT61590/761591) comprise a series of defined structural domain repeats
 CC and/or a RING finger domain; in particular, at least two of a first
 CC domain repeat (AAW13547 or AAW13548), a second domain repeat (AAW13549 or
 CC AAW13550), and a third domain repeat (AAW13551 or AAW13552) and/or a RING
 CC finger domain (AAW13553 or AAW13554), or a consensus sequences derived
 CC from these human genes. The nucleic acid is used for recombinant prodn.
 CC of human cellular inhibitor of apoptosis protein which modulates
 CC apoptosis regulation. The nucleic acids are useful in therapies where
 CC increased cell-specific apoptosis is desired, e.g. in restinosis,
 CC inflammatory disease states, myocardial infarction, glomerular nephritis,
 CC transplant rejection and infectious diseases, e.g. HIV. They can also be
 CC used in conditions requiring a reduction in apoptosis
 XX Sequence 618 AA;

Query Match 97.8%; Score 393; DB 2; Length 618;
 Best Local Similarity 98.5%; Pred. No. 1.1e-37;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 60
 |||||
 Db 269 HAARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 328
 |||||
 QY 61 WPRCEFL 68
 |||||
 Db 329 WPRCEFL 336

RESULT 10
 ABP72160
 ID ABP72160 standard; protein; 618 AA.
 XX
 AC ABP72160;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Human inhibitor of apoptosis protein XIAP.
 XX

Db 329 WPRCEFL 336

RESULT 9
 AAY33998

ID AAY33998 standard; protein; 618 AA.

XX
 AC AAY33998;

XX
 DT 26-NOV-1999 (first entry)

XX
 DE Human cellular inhibitor of apoptosis-1 sequence.

XX
 KW Cellular Inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;
 KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation.

XX
 OS Homo sapiens.

XX
 PN US958772-A.

XX
 PD 28-SEP-1999.

XX
 PF 03-DEC-1998; 98US-00205204.

XX
 PR 03-DEC-1998; 98US-00205204.

XX
 PA (ISIS-) ISIS PHARM INC.

XX
 PI Bennett CF, Cowse LM, Ackermann EJ;

XX
 DR WPI; 1999-561047/47.

XX
 DR N-PSDB; AAZ22143.

XX
 PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1
 PT useful for e.g. diagnostics, therapeutics, and as research reagents.

XX
 PS Example 13; Col 41-46; 32pp; English.

XX
 CC The invention provides antisense compounds of 8-30 nucleotides that
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-1 (c-IAP-
 CC 1). The antisense compounds may be used for diagnostics, therapeutics
 CC (for modulating the expression of c-IAP-1), prophylaxis (e.g. to prevent
 CC or delay infection, inflammation, or tumor formation), as research
 CC reagents (e.g. to distinguish between members of a biological pathway)
 CC and in kits. The present sequence represents the human cellular inhibitor
 CC of apoptosis-1
 XX

SQ Sequence 618 AA;

Query Match 97.8%; Score 393; DB 2; Length 618;
 Best Local Similarity 98.5%; Pred. No. 1.1e-37;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 60
 |||||

Db 269 HAARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 328
 |||||

QY 61 WPRCEFL 68
 |||||

Db 329 WPRCEFL 336

RESULT 10
 ABP72160

ID ABP72160 standard; protein; 618 AA.

XX
 AC ABP72160;

XX
 DT 22-APR-2003 (first entry)

XX
 DE Human inhibitor of apoptosis protein XIAP.

XX

KW Inhibitor of apoptosis; XIAP; human; apoptosis; cancer; leukaemia;
KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003004606-A2.
XX 16-JAN-2003.
XX 03-JUL-2002; 2002WO-US021002.
XX 03-JUL-2001; 2001US-00898158.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX PA Troy CM, Shelanski ML;
XX PI WPI; 2003-210351/20.
XX DR N-PSDB; ABZ58105.
XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
XX treating cancer, neurodegenerative disorder or cardiomyopathy.
XX Disclosure; Fig 18A; 124pp; English.
XX The present sequence is the protein sequence of human inhibitor of
XX apoptosis protein XIAP. The invention provides a nucleic acid, such as an
XX antisense oligonucleotide, which specifically hybridises to a nucleic
XX acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,
XX MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
XX death comprises contacting the cell with the nucleic acid under
XX conditions permitting the nucleic acid to enter the cell, especially the
XX use of a vector, liposome, or a mechanical or electrical means. The
XX method is used to treat acute lymphocytic leukaemia, acute myelogenous
XX leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
XX lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
XX cell carcinoma and squamous cell carcinoma (all claimed)
XX
SQ Sequence 618 AA;
Query Match 97.8%; Score 393; DB 6; Length 618;
Best Local Similarity 98.5%; Pred. No. 1.1e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 328
QY 61 WFPRCFEL 68
Db 329 WFPRCFEL 336
RESULT 11
ADB80949
ID ADB80949 standard; protein; 618 AA.
XX ADB80949;
XX 04-DEC-2003 (first entry)
XX RING-SH complex related protein, SEQ ID No 23.
XX RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
XX Hsp70; Hsp90; STAM1; STAM2B; VHS-UIIM; GTPase; E2 enzyme; tsgr101;
XX cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
XX rhabdovirus; filovirus.
XX Unidentified.
XX WO2003033646-A2.
XX 24-APR-2003.

XX 31-JUL-2002; 2002WO-US024589.
XX 31-JUL-2001; 2001US-0308958P.
XX 09-NOV-2001; 2001US-0345846P.
XX (PROT-) PROTEOLOGICS INC.
XX Greener T, Moskowitz H, Reiss V, Alroy I;
XX WPI; 2003-393509/37.
XX N-PSDB; ADB80990.
XX New isolated protein complex comprising a RING-SH 3 polypeptide and
XX another polypeptide, useful for detecting cells infected with a virus,
XX and for treating viral disorders caused by retroviruses, rhabdoviruses,
XX or filoviruses.
XX Example 2; Fig 23; 176pp; English.
XX The invention relates to a novel isolated protein complex comprising a
XX RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
XX Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
XX STAM2B, VHS-UIIM, a GTPase, an E2 enzyme, tsgr101, a cullin, RING-SH, and a
XX clathrin. The novel protein complex has virucide activity and can be used
XX to treat disorders as part of a vaccine. The protein complex and
XX composition are useful for detecting cells infected with a virus, for
XX identifying agents having antiviral activity, and for treating viral
XX disorders caused by retroviruses, rhabdoviruses, or filoviruses. This
XX sequence is a protein comprising the RING-SH complex of the invention.
XX
SQ Sequence 618 AA;
Query Match 97.8%; Score 393; DB 7; Length 618;
Best Local Similarity 98.5%; Pred. No. 1.1e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGDCGLRCWESGDDPWVEHAK 328
QY 61 WFPRCFEL 68
Db 329 WFPRCFEL 336
RESULT 12
ABR84600
ID ABR84600 standard; protein; 618 AA.
XX ABR84600;
XX 18-DEC-2003 (first entry)
XX IAP1 protein.
XX IAP1; inflammatory response; rheumatoid arthritis; IrbetaR;
XX lymphotoxin-beta receptor; modulator; cancer; immunological disease;
XX apoptosis; cytostatic; immunosuppressive; antirheumatic; antiarthritic;
XX antiinflammatory; dermatological; nephrotropic; antithyroid;
XX thymimetic; muscular-Gen; neuroprotective; antianaemic; haemostatic;
XX vasotropic; antidiabetic.
XX Unidentified.
XX WO2003066834-A2.
XX 14-AUG-2003.
XX 10-FEB-2003; 2003WO-US003923.
XX 08-FEB-2002; 2002US-0355183P.
XX

PA (AMHP) WYETH.
XX
PI Kuai J, Wooters JL, Nickbarg EB, Qiu Y, Lin L;
XX
DR WPI; 2003-748125/70.
XX
XX
PT New purified lymphotoxin-beta receptor protein complex, useful for
PT identifying modulators of lymphotoxin-beta receptor activity or
PT expression for treating or preventing cancer or an autoimmune disorder,
PT e.g. vasculitis or diabetes.
XX
XX
PS Disclosure; Page 7; Opp; English.
XX
XX The present invention relates to a purified complex comprising a
CC lymphotoxin beta receptor (LTbetar) polypeptide and Smac polypeptide. The
CC lymphotoxin-beta receptor (LTbetar) complex is useful for identifying
CC modulators of LTbetar activity or expression for treating or preventing
CC cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid
CC arthritis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's
CC disease, Hashimoto's thyroiditis, pemphigus vulgaris, myasthenia gravis,
CC scleroderma, autoimmune haemolytic anaemia, autoimmune thrombocytopenic
CC purpura, polymyositis, dermatomyositis, pernicious anaemia, Sjogren's
CC syndrome, ankylosing spondylitis, vasculitis, or type I diabetes
CC mellitus. The present sequence is an IAP1 protein, which forms part of
CC the complex of the invention
XX
SQ Sequence 618 AA;
Query Match 97.8%; Score 393; DB 7; Length 618;
Best Local Similarity 98.5%; Pred. No. 1.le-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDVKFCGCGGLRCWESGDDPWVHAK 60
DB 269 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDVKFCGCGGLRCWESGDDPWVHAK 328
QY 61 WPPRCEFL 68
DB 329 WPPRCEFL 336
RESULT 13
ADD25639
ID ADD25639 standard; protein; 618 AA.
AC ADD25639;
XX
XX 15-JAN-2004 (first entry)
XX
XX Binding domain-immunoglobulin fusion protein-associated protein #97.
XX Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
XX US2003118592-A1.
XX
XX 26-JUN-2003.
XX
XX 25-JUL-2002; 2002US-00207655.
XX
XX 17-JAN-2001; 2001US-0367358P.
XX 17-JAN-2002; 2002US-00053530.
XX 03-JUN-2002; 2002US-0395691P.
XX
XX (GENE-) GENE-CRAFT INC.
PA

XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
DR WPI; 2003-801317/75.
XX
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
XX
PS Disclosure; SEQ ID NO 200; 157pp; English.
XX
XX The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 618 AA;
Query Match 97.8%; Score 393; DB 7; Length 618;
Best Local Similarity 98.5%; Pred. No. 1.le-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDVKFCGCGGLRCWESGDDPWVHAK 60
DB 269 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDVKFCGCGGLRCWESGDDPWVHAK 328
QY 61 WPPRCEFL 68
DB 329 WPPRCEFL 336
RESULT 14
ADG10748
ID ADG10748 standard; protein; 618 AA.
XX
XX ADG10748;
XX

DT 26-FEB-2004 (first entry)
 XX Human STAT6-activating protein, SEQ ID NO:338.
 XX
 XX
 XX Human; STAT6-activating protein; drug screening; activator; inhibitor;
 KW allergic disease; inflammation; autoimmune disease; diabetes;
 KW hyperlipidaemia; cancer; infection; HIV infection;
 KW human immunodeficiency; cancer; Th1 hyperfunction; antiallergic;
 KW antiinflammatory; antidiabetic; antilipidemic; antineoplastic; anti-HIV;
 KW cytostatic.; gene therapy; antisense therapy; ribozyme therapy.
 XX
 XX Homo sapiens.
 OS
 XX Homo sapiens.
 XX WO200296943-A1.
 PN
 XX
 XX 05-DEC-2002.
 PD
 XX
 XX 22-MAY-2002; 2002WO-JP004949.
 PF
 XX
 XX 25-MAY-2001; 2001JP-00157043.
 PR
 XX 30-AUG-2001; 2001JP-00260681.
 PR
 XX 10-OCT-2001; 2001JP-00313175.
 XX
 XX (ASH) ASH KASEI KOGYO KK.
 PA
 XX
 XX Honda G, Matsuda A, Muramatsu S, Ishizawa K;
 PI
 XX WPI; 2003-140442/13.
 DR
 XX N-PSDB; ADG10747.
 DR
 XX
 XX STAT6-activating proteins and encoded genes, applicable in diagnosis of
 PT and developing drugs to treat allergic diseases, inflammations, e.g. HIV, and
 PT autoimmune diseases, diabetes, hyperlipidaemia, infections e.g. HIV, and
 PT cancer.
 PT
 XX
 PS Claim 1; SEQ ID NO 338; 2080pp; Japanese.
 PS
 XX The invention relates to 242 human STAT6-activating proteins and cDNAs
 CC encoding them (ADG1041-ADG10894) and to sequences with 95% or more
 CC homology to the STAT6-activating proteins and their encoding nucleic
 CC acids. The invention also relates to recombinant vectors and host cells
 CC comprising a STAT6-activating protein-encoding nucleic acid; the
 CC recombinant production of a STAT6-activating protein; an antibody
 CC specific for a STAT6-activating protein; antisense oligonucleotides and
 CC ribozymes targeted to nucleic acids encoding a STAT6-activating protein;
 CC methods of screening for activators or inhibitors of STAT6-activating
 CC proteins; drug compositions comprising a modulator of STAT6-activating
 CC protein activity or expression; and methods of treating patients by
 CC administration of the drug compositions. The STAT6-activating proteins,
 CC nucleic acids encoding them, and modulators of their activity or
 CC expression are useful in the diagnosis and treatment of allergic
 CC diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia,
 CC cancer, infections (e.g., HIV), cancer and disorders associated with Th1
 CC hyperfunction. The present sequence is related to the invention.
 XX
 XX Sequence 618 AA;
 SQ
 Query Match 97.8%; Score 393; DB 7; Length 618;
 Best Local Similarity 98.5%; Pred. No. 1.1e-37;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HAARMFTMYWPSVVPQPEOLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 60
 |||||
 DB 269 HAARMFTMYWPSVVPQPEOLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 328
 |||||
 QY 61 WPPRCFL 68
 |||||
 DB 329 WPPRCFL 336
 |||||
 RESULT 15
 ADP65159
 ID ADP65159 standard; protein; 618 AA.

XX AC
 XX
 DT 12-AUG-2004 (first entry)
 XX
 XX Human baculoviral IAP repeat-containing protein 2, cIAP1, hiap-2.
 DE
 XX
 XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX
 XX Homo sapiens.
 OS
 XX Homo sapiens.
 XX WO2003072827-A1.
 PN
 XX
 XX 04-SEP-2003.
 PD
 XX
 XX 31-OCT-2002; 2002WO-US035433.
 PF
 XX
 XX 31-OCT-2001; 2001US-0336220P.
 PR
 XX
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA
 XX
 XX Hirsch R, Thorton SL;
 PI
 XX WPI; 2003-712740/67.
 DR
 XX GENBANK; NP_001157.
 DR
 XX
 XX Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 PT
 XX
 PS Disclosure; Page; 56pp; English.
 PS
 XX The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 XX
 XX Sequence 618 AA;
 SQ
 Query Match 97.8%; Score 393; DB 7; Length 618;
 Best Local Similarity 98.5%; Pred. No. 1.1e-37;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HAARMFTMYWPSVVPQPEOLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 60
 |||||
 DB 269 HAARMFTMYWPSVVPQPEOLASAGFYVGRNDVKFCGDCGGLRCWESGDDPWVEHAK 328
 |||||
 QY 61 WPPRCFL 68
 |||||
 DB 329 WPPRCFL 336
 |||||

Db 269 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCDCDGLRCWESGDDPWVEHAK 328
Qy 61 WFPRCEFL 68
Db 329 WFPRCEFL 336
|||||

Search completed: October 22, 2004, 11:16:33
Job time : 117.716 secs

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OM protein - protein search, using sw model

Run on: October 22, 2004, 11:08:12 ; Search time 28.9254 Seconds
(without alignments)
155.905 Million cell updates/sec

Title: US-09-654-743-27

Perfect score: 402

Sequence: 1 HAARMTFTWPSVQPE.....ESGDDPWVHAKWFRCEPL 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	100.0	68	US-08-511-485-27	Sequence 27, Appl
2	402	100.0	68	US-09-201-936-27	Sequence 27, Appl
3	402	100.0	68	US-09-011-356-27	Sequence 27, Appl
4	402	100.0	68	US-09-201-932-27	Sequence 27, Appl
5	402	100.0	618	US-08-511-485-8	Sequence 8, Appl
6	402	100.0	618	US-09-212-971-8	Sequence 8, Appl
7	402	100.0	618	US-08-800-929A-8	Sequence 8, Appl
8	402	100.0	618	US-09-617-053A-8	Sequence 8, Appl
9	402	100.0	618	US-09-201-936-8	Sequence 8, Appl
10	402	100.0	618	US-09-011-356-8	Sequence 8, Appl
11	402	100.0	618	US-09-672-717-223	Sequence 23, App
12	402	100.0	618	US-09-201-932-8	Sequence 8, Appl
13	393	97.8	438	PCT-US95-05922A-2	Sequence 2, Appl
14	393	97.8	618	US-08-569-749-2	Sequence 2, Appl
15	393	97.8	618	US-09-069-023-29	Sequence 29, Appl
16	393	97.8	618	PCT-US96-12860-2	Sequence 2, Appl
17	366	91.0	612	US-09-212-971-14	Sequence 14, Appl
18	366	91.0	612	US-08-800-929A-14	Sequence 14, Appl
19	366	91.0	612	US-08-569-749-14	Sequence 14, Appl
20	366	91.0	612	US-09-617-053A-14	Sequence 14, Appl
21	366	91.0	612	PCT-US96-12860-14	Sequence 14, Appl
22	360	89.6	591	US-09-201-936-42	Sequence 42, Appl
23	360	89.6	591	US-09-011-356-42	Sequence 42, Appl
24	360	89.6	591	US-09-672-717-229	Sequence 29, App
25	360	89.6	591	US-09-201-932-42	Sequence 26, Appl
26	340	84.6	68	US-08-511-485-26	Sequence 26, Appl
27	340	84.6	68	US-09-201-936-26	Sequence 26, Appl

28 340 84.6 68 4 US-09-011-356-26 Sequence 26, Appl
29 340 84.6 68 4 US-09-201-932-26 Sequence 26, Appl
30 340 84.6 442 4 US-09-579-692B-58 Sequence 58, Appl
31 340 84.6 604 2 US-08-511-485-6 Sequence 6, Appl
32 340 84.6 604 3 US-09-212-971-6 Sequence 6, Appl
33 340 84.6 604 3 US-08-800-929A-6 Sequence 6, Appl
34 340 84.6 604 3 US-08-569-749-4 Sequence 4, Appl
35 340 84.6 604 3 US-09-617-053A-6 Sequence 6, Appl
36 340 84.6 604 4 US-09-201-936-6 Sequence 6, Appl
37 340 84.6 604 4 US-09-011-356-6 Sequence 6, Appl
38 340 84.6 604 4 US-09-672-717-221 Sequence 221, App
39 340 84.6 604 4 US-09-201-932-6 Sequence 6, Appl
40 340 84.6 604 5 PCT-US96-12860-4 Sequence 6, Appl
41 340 84.6 1140 4 US-09-579-692B-8 Sequence 8, Appl
42 324 80.6 600 3 US-09-212-971-12 Sequence 12, Appl
43 324 80.6 600 3 US-08-800-929A-12 Sequence 12, Appl
44 324 80.6 600 3 US-09-617-053A-12 Sequence 12, Appl
45 318 79.1 602 4 US-09-201-936-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-08-511-485-27
; Sequence 27, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/POCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-27

Query Match 100.0%; Score 402; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 9,1e-42;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 HAARMTFTWPSVQPEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVHAK 60
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Db 1 HAARMRTFMYWPSVPVQPEOLASAGFYVYGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60

QY 61 WFPCEFL 68

Db 61 WFPCEFL 68

RESULT 2

US-09-201-936-27
 ; Sequence 27, Application US/09201936
 ; Patent No. 6541457
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003003
 ; CURRENT APPLICATION NUMBER: US/09/201,936
 ; CURRENT FILING DATE: 1998-12-01
 ; EARLIER APPLICATION NUMBER: 09/011,356
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 68
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-201-936-27

Query Match 100.0%; Score 402; DB 4; Length 68;
 Best Local Similarity 100.0%; Pred. No. 9.1e-42;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTFMYWPSVPVQPEOLASAGFYVYGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
 |||||
 Db 1 HAARMRTFMYWPSVPVQPEOLASAGFYVYGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
 |||||

QY 61 WFPCEFL 68

Db 61 WFPCEFL 68

RESULT 3

US-09-011-356-27
 ; Sequence 27, Application US/09011356A
 ; Patent No. 6656704
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003002
 ; CURRENT APPLICATION NUMBER: US/09/011,356A
 ; CURRENT FILING DATE: 1998-09-14
 ; EARLIER APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27

; LENGTH: 68

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-011-356-27

Query Match 100.0%; Score 402; DB 4; Length 68;
 Best Local Similarity 100.0%; Pred. No. 9.1e-42;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTFMYWPSVPVQPEOLASAGFYVYGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
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 Db 1 HAARMRTFMYWPSVPVQPEOLASAGFYVYGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
 |||||

QY 61 WFPCEFL 68

Db 61 WFPCEFL 68

RESULT 4

US-09-201-932-27
 ; Sequence 27, Application US/09201932A
 ; Patent No. 6689562
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003004
 ; CURRENT APPLICATION NUMBER: US/09/201,932A
 ; CURRENT FILING DATE: 1998-12-01
 ; EARLIER APPLICATION NUMBER: 09/011,356
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 68
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-201-932-27

Query Match 100.0%; Score 402; DB 4; Length 68;
 Best Local Similarity 100.0%; Pred. No. 9.1e-42;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTFMYWPSVPVQPEOLASAGFYVYGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
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 Db 1 HAARMRTFMYWPSVPVQPEOLASAGFYVYGRNDDVKFCGDCGLRCWESGDDPWVEHAK 60
 |||||

QY 61 WFPCEFL 68

Db 61 WFPCEFL 68

RESULT 5

US-08-511-485-8
 ; Sequence 8, Application US/08511485
 ; Patent No. 5918912
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:


```
/
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/511,485
/ FILING DATE: 04-AUG-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 07540/002001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 618 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: both
/ MOLECULE TYPE: protein
/ US-08-511-485-8
/
/ Query Match 100.0%; Score 402; DB 2; Length 618;
/ Best Local Similarity 100.0%; Pred. No. 1.1e-40;
/ Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 HAARMRTFMYWSSVPVQPEQLASAGFYVVGNDVKFCGDCGGLRCWESGDDPWVEHAK 60
/ Db 269 HAARMRTFMYWSSVPVQPEQLASAGFYVVGNDVKFCGDCGGLRCWESGDDPWVEHAK 328
/
/ QY 61 WPPRCEFL 68
/ Db 329 WPPRCEFL 336
/
/ RESULT 6
/ US-09-212-971-8
/ Sequence 8, Application US/09212971B
/ Patent No. 6107041
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G
/ APPLICANT: Mackenzie, Alexander E
/ APPLICANT: Liston, Peter
/ APPLICANT: Baird, Stephen
/ APPLICANT: Tsang, Benjamin K
/ APPLICANT: Pratt, Christine
/ TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
/ TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
/ TITLE OF INVENTION: DISEASE
/ FILE REFERENCE: 07891/009002
/ CURRENT APPLICATION NUMBER: US/09/212,971B
/ CURRENT FILING DATE: 1998-12-16
/ EARLIER APPLICATION NUMBER: 60/017,354
/ EARLIER FILING DATE: 1996-04-26
/ EARLIER APPLICATION NUMBER: 60/030,590
/ EARLIER FILING DATE: 1996-11-14
/ EARLIER APPLICATION NUMBER: 08/800,929
/ EARLIER FILING DATE: 1997-02-13
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 618
/ TYPE: PRT
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/ ORGANISM: Homo sapiens
/ US-09-212-971-8
/
/ Query Match 100.0%; Score 402; DB 3; Length 618;
/ Best Local Similarity 100.0%; Pred. No. 1.1e-40;
/ Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 HAARMRTFMYWSSVPVQPEQLASAGFYVVGNDVKFCGDCGGLRCWESGDDPWVEHAK 60
/ Db 269 HAARMRTFMYWSSVPVQPEQLASAGFYVVGNDVKFCGDCGGLRCWESGDDPWVEHAK 328
/
/ QY 61 WPPRCEFL 68
/ Db 329 WPPRCEFL 336
/
/ RESULT 7
/ US-08-800-929A-8
/ Sequence 8, Application US/08800929A
/ Patent No. 6133437
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G
/ APPLICANT: Mackenzie, Alexander E
/ APPLICANT: Liston, Peter
/ APPLICANT: Baird, Stephen
/ APPLICANT: Tsang, Benjamin K
/ APPLICANT: Pratt, Christine
/ TITLE OF INVENTION: DETECTION AND MODULATION OF
/ TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
/ TITLE OF INVENTION: DISEASE
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Clark & Elbing LLP
/ STREET: 176 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/800,929A
/ FILING DATE: 13-FEB-1997
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/030,590
/ FILING DATE: 14-NOV-1996
/ APPLICATION NUMBER: 60/017,354
/ FILING DATE: 26-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bieker-Brady, Kristina
/ REGISTRATION NUMBER:
/ REFERENCE/DOCKET NUMBER: 07891/009001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-428-0200
/ TELEFAX: 617-428-7045
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 618 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-800-929A-8
/
/ Query Match 100.0%; Score 402; DB 3; Length 618;
/ Best Local Similarity 100.0%; Pred. No. 1.1e-40;
/ Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-672-717-223

Query Match
Best Local Similarity 100.0%; Score 402; DB 4; Length 618;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 269 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDVVKFCGDCGLRCWESGDDPWVEHAK 328

QY 61 WFPRCFEL 68
Db 329 WFPRCFEL 336

RESULT 12
US-09-201-932-8
; Sequence 8, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-8

Query Match
Best Local Similarity 100.0%; Score 402; DB 4; Length 618;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDVVKFCGDCGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDVVKFCGDCGLRCWESGDDPWVEHAK 328

QY 61 WFPRCFEL 68
Db 329 WFPRCFEL 336

RESULT 13
PCT-US95-05922A-2
; Sequence 2, Application PC/TUS9505922A
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; NUMBER OF SEQUENCES: 8
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05922A
; FILING DATE: 11 MAY 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-292
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
PCT-US95-05922A-2

Query Match
Best Local Similarity 97.8%; Score 393; DB 5; Length 438;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 89 HAARMRTFMYWPSVPVQPEQLASAGFYVYVGRNDVVKFCGDCGLRCWESGDDPWVEHAK 148

QY 61 WFPRCFEL 68
Db 149 WFPRCFEL 156

RESULT 14
US-08-569-749-2
; Sequence 2, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
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; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-749-2

Query Match          97.8%; Score 393; DB 3; Length 618;
Best Local Similarity 98.5%; Pred. No. 1.4e-39;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      269 HAARMRTFMWPSVPVQPEQLASAGFYVYGRNDVKCFCDGGLRCWESGDDPWVEHAK 328

QY      61 WPPRCEFL 68
      |||||||
Db      329 WPPRCEFL 336

RESULT 15
US-09-069-023-29
; Sequence 29, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-29

Query Match          97.8%; Score 393; DB 3; Length 618;
Best Local Similarity 98.5%; Pred. No. 1.4e-39;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      269 HAARMRTFMWPSVPVQPEQLASAGFYVYGRNDVKCFCDGGLRCWESGDDPWVEHAK 328

QY      61 WPPRCEFL 68
      |||||||
Db      329 WPPRCEFL 336

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Job time : 28.9254 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 11:21:03 ; Search time 87.2836 Seconds
(without alignments)
252.231 Million cell updates/sec

Title: US-09-654-743-27

Perfect score: 402

Sequence: 1 HAARMETFWPSSVQPE.....ESGDDPWVEHAKWPRCEFL 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pep:*
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- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	100.0	68	9	US-09-201-936-27
2	402	100.0	68	16	US-10-600-272-27
3	402	100.0	618	9	US-09-974-592-8
4	402	100.0	618	9	US-09-201-936-8
5	402	100.0	618	16	US-10-636-065-223
6	402	100.0	618	16	US-10-600-272-8
7	393	97.8	438	8	US-08-464-588-2
8	393	97.8	438	14	US-10-323-643-2
9	393	97.8	618	14	US-10-153-668-338
10	393	97.8	618	14	US-10-207-655-200
11	393	97.8	618	14	US-10-232-286-2
12	393	97.8	618	14	US-10-366-307-4
13	393	97.8	618	15	US-10-361-270-3

14	393	97.8	618	15	US-10-260-708-63	Sequence 63, Appl
15	393	97.8	618	16	US-10-730-476A-78	Sequence 78, Appl
16	366	91.0	612	9	US-09-974-592-14	Sequence 14, Appl
17	366	91.0	612	14	US-10-232-286-14	Sequence 14, Appl
18	360	89.6	591	9	US-09-201-936-42	Sequence 42, Appl
19	360	89.6	591	16	US-10-636-065-229	Sequence 229, App
20	360	89.6	591	16	US-10-600-272-42	Sequence 42, Appl
21	340	84.6	68	9	US-09-201-936-26	Sequence 26, Appl
22	340	84.6	68	16	US-10-600-272-26	Sequence 26, Appl
23	340	84.6	604	9	US-09-974-592-6	Sequence 6, Appl
24	340	84.6	604	9	US-09-201-936-6	Sequence 6, Appl
25	340	84.6	604	14	US-10-232-286-4	Sequence 4, Appl
26	340	84.6	604	14	US-10-141-618-6	Sequence 6, Appl
27	340	84.6	604	14	US-10-366-307-6	Sequence 6, Appl
28	340	84.6	604	16	US-10-636-065-221	Sequence 221, App
29	340	84.6	604	16	US-10-600-272-6	Sequence 6, Appl
30	340	84.6	604	16	US-10-730-476A-79	Sequence 79, Appl
31	340	84.6	1140	14	US-10-353-461-8	Sequence 8, Appl
32	324	80.6	600	9	US-09-974-592-12	Sequence 12, Appl
33	318	79.1	602	9	US-09-201-936-40	Sequence 40, Appl
34	318	79.1	602	16	US-10-636-065-227	Sequence 227, App
35	318	79.1	602	16	US-10-600-272-40	Sequence 40, Appl
36	283	70.4	48	14	US-10-232-286-9	Sequence 9, Appl
37	270	67.2	48	14	US-10-232-286-10	Sequence 10, Appl
38	250	62.2	50	14	US-10-138-618-31	Sequence 31, Appl
39	234	58.2	68	9	US-09-201-936-28	Sequence 28, Appl
40	234	58.2	68	14	US-10-041-859-18	Sequence 18, Appl
41	234	58.2	68	16	US-10-600-272-28	Sequence 28, Appl
42	234	58.2	172	14	US-10-041-859-12	Sequence 12, Appl
43	234	58.2	268	14	US-10-323-643-10	Sequence 10, Appl
44	232	57.7	280	14	US-10-244-586-3	Sequence 3, Appl
45	232	57.7	280	17	US-10-807-897-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-09-201-936-27
; Sequence 27, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; CURRENT APPLICATION NUMBER: US/09/003003
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-27

Query Match 100.0%; Score 402; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 5,1e-39;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMETFWPSSVQPEQLASGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAK 60
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DB 1 HAARMRTFMYPSSVPVQPEQLASAGFYVYVGRNDVKFCGCDGGLRCWESGDDPWVEHAK 60
 QY 61 WFPRCFEL 68
 DB 61 WFPRCFEL 68
 RESULT 2
 US-10-600-272-27
 ; Sequence 27, Application US/10600272
 ; Publication No. US20040157232A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003006
 ; CURRENT APPLICATION NUMBER: US/10/600,272
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 09/011,356
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: PCT/IB96/01022
 ; PRIOR FILING DATE: 1996-08-05
 ; PRIOR APPLICATION NUMBER: US 08/576,956
 ; PRIOR FILING DATE: 1995-12-22
 ; PRIOR APPLICATION NUMBER: US 08/511,495
 ; PRIOR FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 68
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-600-272-27
 Query Match 100.0%; Score 402; DB 16; Length 68;
 Best Local Similarity 100.0%; Pct. No. 5,1e-39;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HAARMRTFMYPSSVPVQPEQLASAGFYVYVGRNDVKFCGCDGGLRCWESGDDPWVEHAK 60
 DB 1 HAARMRTFMYPSSVPVQPEQLASAGFYVYVGRNDVKFCGCDGGLRCWESGDDPWVEHAK 60
 QY 61 WFPRCFEL 68
 DB 61 WFPRCFEL 68
 RESULT 3
 US-09-974-592-8
 ; Sequence 8, Application US/09974592
 ; Patent No. US20020120121A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; TITLE OF INVENTION: DISEASE
 ; FILE REFERENCE: 07891/009004
 ; CURRENT APPLICATION NUMBER: US/09/974,592
 ; CURRENT FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: US 09/617,053
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/800,929
 ; PRIOR FILING DATE: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0

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; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-636-065-223

Query Match      100.0%; Score 402; DB 16; Length 618;
Best Local Similarity 100.0%; Pred. No. 4.8e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 269 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 328
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QY 61 WPPRCEFL 68
   |||||
Db 329 WPPRCEFL 336
   |||||

RESULT 6
US-10-600-272-8
; Sequence 8, Application US/10600272
; Publication No. US20040157322A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-8

Query Match      100.0%; Score 402; DB 16; Length 618;
Best Local Similarity 100.0%; Pred. No. 4.8e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 60
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Db 269 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 328
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QY 61 WPPRCEFL 68
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Db 329 WPPRCEFL 336
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RESULT 7
US-08-464-588-2
; Sequence 2, Application US/08464588
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; Publication No. US20030073159A1
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,588
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05922
; FILING DATE: 11 MAY 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-464-588-2

Query Match      97.8%; Score 393; DB 8; Length 438;
Best Local Similarity 98.5%; Pred. No. 3.8e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 60
   |||||
Db 89 HAARMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 148
   |||||

QY 61 WPPRCEFL 68
   |||||
Db 149 WPPRCEFL 156
   |||||

RESULT 8
US-10-323-643-2
; Sequence 2, Application US/10323643
; Publication No. US20030108552A1
; GENERAL INFORMATION:
; APPLICANT: He, et al.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; FILE REFERENCE: PFI65P1D1
; CURRENT APPLICATION NUMBER: US/10/323,643
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 08/464,588
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US95/05922
; PRIOR FILING DATE: 1995-05-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 438
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-323-643-2

Query Match          97.8%; Score 393; DB 14; Length 438;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 60
    |||||||
Db 89 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 148
    |||||||

QY 61 WFPCEFL 68
    |||||||
Db 149 WFPCEFL 156

RESULT 9
US-10-153-668-338
; Sequence 338, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 338
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-338

Query Match          97.8%; Score 393; DB 14; Length 618;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 60
    |||||||
Db 269 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 328
    |||||||

QY 61 WFPCEFL 68
    |||||||
Db 329 WFPCEFL 336

RESULT 10
US-10-207-655-200
; Sequence 200, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
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; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 200
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-200

Query Match          97.8%; Score 393; DB 14; Length 618;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 60
    |||||||
Db 269 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 328
    |||||||

QY 61 WFPCEFL 68
    |||||||
Db 329 WFPCEFL 336

RESULT 11
US-10-232-286-2
; Sequence 2, Application US/10232286
; Publication No. US20030143579A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,286
; FILING DATE: 30-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-232-286-2

Query Match          97.8%; Score 393; DB 14; Length 618;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 60
    |||||||
Db 269 HAARMRTMYWPSVPVQPEQLASAGFYVYVGRNDDVKFCGCDGGLRCWESGDDPWVEHAK 328
    |||||||
```



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QY 61 WPCRCEFL 68
Db 329 WPCRCEFL 336

RESULT 12
US-10-366-307-4
; Sequence 4, Application US/10366307
; Publication No. US20030224399A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Determining the Prognosis
; FILE REFERENCE: P-LJ 5659
; CURRENT APPLICATION NUMBER: US/10/366,307
; PRIOR APPLICATION NUMBER: 2003-02-12
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-307-4

Query Match 97.8%; Score 393; DB 14; Length 618;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 328

QY 61 WPCRCEFL 68
Db 329 WPCRCEFL 336

RESULT 13
US-10-361-270-3
; Sequence 3, Application US/10361270
; Publication No. US20040038299A1
; GENERAL INFORMATION:
; APPLICANT: Kuai, Jun
; APPLICANT: Wooters, Joseph L
; APPLICANT: Nickbarg, Elliott
; APPLICANT: Qiu, Yongchang
; APPLICANT: Lin, Lih-Ling
; TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
; FILE REFERENCE: 22058-565
; CURRENT APPLICATION NUMBER: US/10/361,270
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/355,183
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-270-3

Query Match 97.8%; Score 393; DB 15; Length 618;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 328

QY 61 WPCRCEFL 68
Db 329 WPCRCEFL 336

RESULT 14
US-10-260-708-63
; Sequence 63, Application US/10260708
; Publication No. US20040063101A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Lee, Sang-Yull
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Human Sarcoma-Associated Antigens
; FILE REFERENCE: L00461/70138
; CURRENT APPLICATION NUMBER: US/10/260,708
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 618
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-260-708-63

Query Match 97.8%; Score 393; DB 15; Length 618;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 328

QY 61 WPCRCEFL 68
Db 329 WPCRCEFL 336

RESULT 15
US-10-730-476A-78
; Sequence 78, Application US/10730476A
; Publication No. US20040171105A1
; GENERAL INFORMATION:
; APPLICANT: Du, Chunying
; APPLICANT: Yang, Qiheng
; TITLE OF INVENTION: Method and Composition for Cleaving IAPs
; FILE REFERENCE: 40716(IP-022)
; CURRENT APPLICATION NUMBER: US/10/730,476A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-730-476A-78

Query Match 97.8%; Score 393; DB 16; Length 618;
Best Local Similarity 98.5%; Pred. No. 5.3e-37;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTMYWPSVPVQPEQLASAGFYVGRNDDVKFCGDCGGLRCWESGDDPWVEHAK 328

QY 61 WPCRCEFL 68
Db 329 WPCRCEFL 336

Search completed: October 22, 2004, 11:37:10
Job time : 88.2836 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 11:08:02 ; Search time 23.8507 Seconds
(without alignments)
274.320 Million cell updates/sec

Title: US-09-654-743-27

Perfect score: 402

Sequence: 1 HAARMRTFMYWPSVVPQPE.....ESGDDPWVHAKWFPRCFEL 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	618	2 S68450	apoptosis inhibito
2	342	85.1	358	2 JC5964	apoptosis inhibito
3	340	84.6	604	2 S68449	apoptosis inhibito
4	234	58.2	268	2 T10304	inhibitor of apopt
5	234	58.2	268	2 A53989	apoptosis-inhibiti
6	232	57.7	298	2 JC7568	kidney inhibitor o
7	218	54.2	275	2 A45679	inhibitor-of-apopt
8	212.5	52.9	1232	2 A55478	neuronal apoptosis
9	208.5	51.9	1447	2 T42628	apoptosis inhibito
10	198	49.3	496	2 S68452	apoptosis inhibito
11	198	49.3	497	2 S69544	apoptosis inhibito
12	198	49.3	497	2 S69544	apoptosis inhibito
13	149	37.1	275	2 T10310	apoptosis inhibiti
14	148	36.8	150	2 T28409	apoptosis-inhibiti
15	147.5	36.7	286	2 D36828	ORF MSV248 probabl
16	144.5	35.9	292	2 T41772	orf13 protein - Au
17	139.5	34.7	4845	2 T31067	IAP1 orf27 - Bomby
18	132	32.8	208	2 T03183	BIR repeat contain
19	119.5	29.7	997	2 T43523	probable apoptosis
20	118	29.4	155	2 T30489	cut17 protein-ori
21	85	21.1	155	2 T37471	apoptosis inhibito
22	84	20.9	308	2 T37474	apoptosis inhibito
23	81	20.1	234	2 T30427	apoptosis inhibito
24	80.5	20.0	329	2 T28403	probable apoptosis
25	74	18.4	249	2 H72858	ORF MSV242 probabl
26	71	17.7	249	2 T41814	apoptosis inhibito
27	66.5	16.5	951	1 SYECTV	IAP2 orf71 - Bomby
28	65.5	16.3	951	2 C91283	valine-tRNA synthet
29	65.5	16.3	951	2 E86124	valine tRNA synthet

ALIGNMENTS

RESULT 1

S68450

apoptosis inhibitor hiap-2 - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: S68450

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,

Nature 379, 349-353, 1996

A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP

A:Reference number: A56182; MUID:96149249; PMID:8552191

A:Accession: S68450

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-618 <LIS>

A:Cross-references: UNIPROT:Q13490; EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g118

C:Function:

A:Description: apoptotic suppressor

C:Keywords: apoptosis; zinc finger

F:567-611/Domain: RING finger homology <RNG>

Query Match 100.0%; Score 402; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 5.8e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAARMRTFMYWPSVVPQPEQLASAGFYVGRNDVKCFGGDGLRCWESGDDPWVHAK 60

Db 269 HAARMRTFMYWPSVVPQPEQLASAGFYVGRNDVKCFGGDGLRCWESGDDPWVHAK 328

QY 61 WFPRCFEL 68

Db 329 WFPRCFEL 336

RESULT 2

JC5964

apoptosis inhibitor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004

C:Accession: JC5964

R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.

Biochem. Biophys. Res. Commun. 243, 827-832, 1998

A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (iap) fam

A:Reference number: JC5964; MUID:98162622; PMID:9501011

A:Accession: JC5964

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: UNIPROT:O62640; GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g29571

F:307-351/Domain: RING finger homology <RRN>

Query Match

Best Local Similarity 85.1%; Score 342; DB 2; Length 358;
Pred. No. 2.3e-31;

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Matches 56; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 1 HAARMRTFMWPSVPVQPEQLASAGFYVVGRRNDVKFCGCGGLRCWESGDDPWVEHAK 60
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90 YAAARFKTFCNWPFSSIPVHPEQLASAGFYVVGRRNDVKFCGCGGLRCWESGDDPWVEHAK 149
QY 61 WPRCEFL 68
:|||||:
Db 150 WPRCEYL 157

RESULT 3
S68449
apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIN>
A:Cross-references: UNIPROT:Q13489; EMBL:U45878; NID:g1184315; PID:g118
C:Function:
A:Description: apoptotic suppressor
C:Keywords: apoptosis; zinc finger
F:553-597/Domain: RING finger homology <RNG>

Query Match 84.6%; Score 340; DB 2; Length 604;
Best Local Similarity 83.8%; Pred. No. 6.5e-31; Indels 0; Gaps 0;
Matches 57; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 HAARMRTFMWPSVPVQPEQLASAGFYVVGRRNDVKFCGCGGLRCWESGDDPWVEHAK 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
255 HAARFKTFNWPSVVLNPEQLASAGFYVVGRRNDVKFCGCGGLRCWESGDDPWVQHAK 314
QY 61 WPRCEFL 68
:|||||:
Db 315 WPRCEYL 322

RESULT 4
T10304
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T10304
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10304
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <AHR>
A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match 58.2%; Score 234; DB 2; Length 268;
Best Local Similarity 53.7%; Pred. No. 3.4e-19; Indels 0; Gaps 0;
Matches 36; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
QY 2 AARMRTFMWPSVPVQPEQLASAGFYVVGRRNDVKFCGCGGLRCWESGDDPWVEHAK 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
112 AARLRTFAEWPRGLKQRPPELAEAGFFYTGQDKTRCFCCDGLKDWEPDAPWQHARW 171
QY 62 FPRCEFL 68
:|||||:
Db 172 YDRCEYL 178

RESULT 5
A53989
apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis vir
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53989
R:Binbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a poly
A:Reference number: A53989; MUID:94187094; PMID:8139034
A:Accession: A53989
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <BIR>
A:Cross-references: UNIPROT:P41437; GB:L22564; NID:g456111; PIDN:AAB02610.1; PID:g4561114
A>Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as As
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match 58.2%; Score 234; DB 2; Length 268;
Best Local Similarity 53.7%; Pred. No. 3.4e-19; Indels 0; Gaps 0;
Matches 36; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
QY 2 AARMRTFMWPSVPVQPEQLASAGFYVVGRRNDVKFCGCGGLRCWESGDDPWVEHAKW 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
112 AARLRTFAEWPRGLKQRPPELAEAGFFYTGQDKTRCFCCDGLKDWEPDAPWQHARW 171
QY 62 FPRCEFL 68
:|||||:
Db 172 YDRCEYL 178

RESULT 6
JC7568
kidney inhibitor of apoptosis protein - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7568
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A:Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.
A:Reference number: JC7568; MUID: 21092523; PMID:11162435
A:Contents: Fetal kidney
A:Accession: JC7568
A:Molecule type: mRNA
A:Residues: 1-298 <LIN>
A:Cross-references: UNIPROT:Q96CA5
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, play
C:Genetics:
A:Gene: kiap
A:Map position: 20q13.3
C:Keywords: apoptosis

Query Match 57.7%; Score 232; DB 2; Length 298;
Best Local Similarity 56.9%; Pred. No. 6.4e-19; Indels 0; Gaps 0;
Matches 37; Conservative 10; Mismatches 18; Indels 0; Gaps 0;
QY 4 RMRTFMWPSVPVQPEQLASAGFYVVGRRNDVKFCGCGGLRCWESGDDPWVEHAKWFP 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90 RLASFYDWPLTAEPPELLAAAGFFHTGHQDKVRCFCFCYGLQSKRGKDDPWTEHAKWFP 149
Db 64 RCEFL 68
:|||||:
QY 150 SCQFL 154
Db 150 SCQFL 154

RESULT 7
A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C:Species: Cydia pomonella granulosis virus CpGV
```

[illegible]

RESULT 8
A55478
neuronal apoptosis inhibitory protein - human
C:Species: Homo sapiens (man)
N:Alternate names: NAIP
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C:Accession: A55478
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Varaghi, Z.; Farahani, R.; Baird, S.
d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.
Cell 80, 167-178, 1995
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi
A:Reference number: A55478; MUID:95112344; PMID:7813013
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <ROY>
A:Cross-references: GB:U19251
C:Genetics:
A:Gene: GDB:SMA@; SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot
F:94-110/Domain: transmembrane #status predicted <TM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted <TM2>
F:476/Binding site: ATP [lys] #status predicted
F:618, 632, 823, 923, 1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match      52.9%; Score 212.5; DB 2; Length 1232;
Best Local Similarity 55.2%; Pred. No. 4.4e-16;
Matches 37; Conservative 8; Mismatches 21; Indels 1; Gaps 1

QY   3 ARMRTFTWVPSVP-VQEQLASAGFYVGRNDVKFCGDCGLRCWESGDGDPVVEHAKW 61
    |||:|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   161 ARLASFRRNPFYVGQISFVLSEAGFVTKGTQTVQCFCGGCLGNWERGGDPPWEHAKW 220
                                     |||::|::|::|::|::|::|
QY   62 FPRCEFL 68
    |||::|::|::|::|::|::|
Db   221 FPKCFEL 227
```

RESULT 9
T42628
neuronal apoptosis inhibitory protein 2 - mouse
C:Species: Mus musculus (house mouse)
C:date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42628

R;Yaraghi, Z.; Diez, E.; Gros, P.; MacKenzie, A.
Mamm. Genome 10, 761-763, 1999
A;Title: CDNA cloning and the 5'genomic organization of Naip2, a candidate gene for murine
A;Reference number: Z22179; MUID:93315342; PMID:10384056
A;Accession: Y24628
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1447 <VAR>
A;Cross-references: UNIPROT:Q9UQK4; EMBL:AF102871; NID:G3860228; PID:G3860229; PIDN:AACT
C;Genetics:
A;Gene: Naip2

Query Match	51.9%;	Score 208.5;	DB 2;	Length 1447;
Best Local Similarity	53.7%;	Pred. No. 1.5e-15;		
Matches	36;	Conservative	9;	Mismatches 21; Indels 1; Gaps 1;
Qy	3	ARMRTMYWP-SSVPVQPEOLASGFYYVGRNDVVKFCGDCGGIRCWESGDDPWPVEHAKW	61	
Db	161	ARLESFEDWPFYAHGTSFVLSAAGFVFTCKRTVQCFCSCGCLGNWEEGDDPWPKEHAKW	220	
Qy	62	FPRCEFL 68		
Db	221	FPKCEFL 227		

RESULT 10
S68452
apoptosis inhibitor diap - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: S68452; S78528
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A;A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP A;Reference number: A58182; MUID:96149249; PMID:8532191
A;Accession: S68452
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-496 <LIS>
A;Cross-references: UNIPROT:Q24307; EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184313
R;Baird, S.D.
submitted to the EMBL Data Library, January 1996
A;Reference number: S78528
A;Accession: S78528
A;Molecule type: mRNA
A;Residues: 1-36, 'A', '37', 'K', '39', 'L', '41-44', 'H', '46-58', 'Q', '60-412', 'A', '414-427', 'A', '429-496 <LIS>
A;Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
C;Genetics:

A:Cross-references: FlyBase:FBgn0015247
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:445-489/Domain: RING finger homology <RNG>

```

Query Match          49.3%; Score 198; DB 2; Length 496;
Best Local Similarity 53.7%; Pred. No. 7.9e-15;
Matches 36; Conservative 9; Mismatches 20; Indels 2; Gaps 2;

QY      3  ARMRFTMYWPSVPVQP-EQLASAGFYYYGRNDVVKCFGCDGGILRCWESGDDPWVEHAKW 61
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      212  ARLRFTFTDWPIS-NIQPASALAQAGLYYQKIQDQVRCFHCNIGLRWQKDEDFWFEHAKW 270

QY      62  FPRCEFL 68
      ||:|:|
Db      271  SPKCOFV 277

```

RESULT 11
S69545
apoptosis inhibitor IAP homolog - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C.Date: 06-Dec-1996 #sequence revision 13-Mar-1997 #text change 09-Jul-2004

C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69545
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
C:Genetics:
A:Gene: ilp
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F:446-490/Domain: RING finger homology <RRN>

Query Match 49.3%; Score 198; DB 2; Length 497;
Best Local Similarity 53.7%; Pred. No. 7.9e-15;
Matches 36; Conservative 9; Mismatches 20; Indels 2; Gaps 2;

QY 3 ARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAKW 61
Db 214 ARLRTFTDWPIS-NIQPASALQAAGLYQKIGDQVRCHFCNTGLRSWQKEDPWFHAKW 272

QY 62 PRCFEL 68
Db 273 SPKQFV 279

RESULT 12
S69544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S69544; S68451
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: UNIPROT:P98170; EMBL:U32974; NID:g1016687; PIDN:AAC50518.1; PID:g101
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:g1184319; PIDN:AAC50373.1; PID:g1184320
C:Genetics:
A:Gene: ilp
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 49.3%; Score 198; DB 2; Length 497;
Best Local Similarity 52.9%; Pred. No. 7.9e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 HAARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAK 60
Db 265 YEARIFTFTGWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEDPWEQHA 322

QY 61 WPRCEFL 68
Db 323 WYPGCKYL 330

RESULT 13

T10310
apoptosis-inhibiting protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OPMNPV
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T10310
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10310
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <AHE>
A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59040.1; PID:g1911287
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:223-268/Domain: RING finger homology <RRN>

Query Match 37.1%; Score 149; DB 2; Length 275;
Best Local Similarity 38.8%; Pred. No. 1.7e-09;
Matches 26; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

QY 2 AARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAKW 61
Db 127 SARRATFDHWPAAALNALTHDAEAGWFTMLGDETACFFDCRVRDLFGDDPWQRHALA 186

QY 62 PRCFEL 68
Db 187 NPQCYFV 193

RESULT 14

T28409
ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomo
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28409
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Cross-references: UNIPROT:Q9YVU4; EMBL:AF063866; NID:g4049647; PIDN:AAC97724.1; PID:g4
A:Genetics:
A>Note: MSV248

Query Match 36.8%; Score 148; DB 2; Length 150;
Best Local Similarity 34.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 3 ARMRTFMWPSVPVQPEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAKW 62
Db 18 SRINSYENWPISLFFKINRLCEAGFFYTNIGDITVCNGLKIKNLYINDPWIEHSKWS 77

QY 63 PRCFEL 68
Db 78 PNCNYI 83

RESULT 15

D36828
orf13 protein - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: D36828; C72853
R:Brannagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
A:Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica
VP8 of rotavirus.
A:Reference number: A44221; MUID:93079853; PMID:1333113

Search completed: October 22, 2004, 11:21:45
Job time : 24.8507 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 10:50:26 ; Search time 128.896 Seconds
(without alignments)
303.544 Million cell updates/sec

Title: US-09-654-743-27

Perfect score: 402

Sequence: 1 HAARMRTFMYWPSVPVQPE.....ESGDDPWVEHAKWFFRCFL 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	393	97.8	534	2	Q81Z20		Q81Z20 homo sapien
2	393	97.8	618	1	B1R2_HUMAN		Q13490 homo sapien
3	366	91.0	612	1	B1R2_MOUSE		Q62210 mus musculu
4	359	89.3	589	2	Q6P6S1		Q6P6S1 rattus norv
5	359	89.3	589	2	AAH62055		Aah62055 rattus no
6	353	87.8	589	2	Q9QZG6		Q9qzc6 rattus norv
7	353	87.8	589	2	Q9ESB8		Q9ese8 rattus norv
8	351	87.3	195	2	Q9IA70		Q9ia70 gallus gall
9	351	87.3	197	2	Q9IA69		Q9ia69 gallus gall
10	351	87.3	611	1	B1R_CHICK		Q90660 gallus gall
11	342	85.1	358	1	PIAF_PIG		Q62640 sus scrofa
12	340	84.6	604	1	B1R3_HUMAN		Q13489 homo sapien
13	334	83.1	604	2	Q6DDY3		Q6ddy3 xenopus lae
14	334	83.1	628	2	Q8UMD2		Q8umd2 brachydanio
15	334	83.1	647	2	Q7TKX2		Q7tkx2 brachydanio
16	334	83.1	654	2	Q6ZM93		Q6zm93 brachydanio
17	334	83.1	654	2	CAE47763		Cae47763 brachydan
18	332	82.6	602	2	Q9ESE9		Q9ese9 rattus norv
19	331	82.3	616	2	Q804E2		Q804e2 ictalurus p
20	327	81.3	604	2	Q6GLD7		Q6glld7 xenopus tro
21	325	80.8	324	2	Q9DDN2		Q9ddn2 gallus gall
22	324	80.6	374	2	Q921N0		Q921n0 mus musculu
23	324	80.6	600	1	B1R3_MOUSE		O08863 mus musculu
24	281	69.9	224	2	O88642		O88642 rattus norv
25	255	63.4	280	2	Q6VTV9		Q6vtv9 choristoneu
26	255	63.4	280	2	AAQ91688		Aaq91688 choristoneu
27	249	61.9	287	2	Q6E7G7		Q6e7g7 anticarsia
28	248	61.7	401	2	Q8JHV9		Q8jhv9 xenopus lae
29	245	60.9	264	2	Q9EN27		Q9en27 amsacta moo
30	241	60.0	269	2	Q6QXJ6		Q6qxj6 agrotis seg
31	241	60.0	269	2	AAS82685		Aas82685 agrotis s

32 238 59.2 281 2 Q9YNL8 Q9ynl8 choristoneu
33 235 58.5 263 2 Q80SF4 Q80sf4 lyphantria
34 234 58.2 268 1 IAP3_NFWOP Iap3 nfwop
35 232 57.7 224 2 Q6R308 Q6r308 homo sapien
36 232 57.7 224 2 AAS01729 Aas01729 homo sapien
37 232 57.7 238 1 B1R7_HUMAN B1r7 human
38 231 57.5 276 2 Q71A73 Q71a73 mamestra co
39 231 57.5 276 2 Q8QL95 Q8ql95 mamestra co
40 231 57.5 276 2 AAQ11158 Aaq11158 mamestra co
41 229 57.0 322 2 Q6DBV7 Q6dbv7 brachydanio
42 229 57.0 346 2 Q8IS31 Q8is31 bombyx mori
43 229 57.0 346 2 Q968T8 Q968t8 bombyx mori
44 229 57.0 405 2 Q8UWH2 Q8uwh2 brachydanio
45 229 57.0 415 2 Q7SXU1 Q7sxu1 brachydanio

ALIGNMENTS

RESULT 1

Q81Z20 PRELIMINARY; PRT; 534 AA.
ID Q81Z20
AC Q81Z20;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE PRB-interacting protein RbBP-36.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Fan Z.S., Ao S.Z.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF207599; AAN73272.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR011029; DEATH_like.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SMO0238; BIR; 3.
DR SMART; SMO0114; CARD; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
SQ SEQUENCE 534 AA; 60366 MW; 0403170475BE0872 CRC64;

Query Match

Best Local Similarity 98.5%; Score 393; DB 2; Length 534;

Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAARMRTFMYWPSVPVQPEQLASAGFYVGRNDDVKFCGCDGLRCWESGDDPWVEHAK 60
Db 269 HAARMRTFMYWPSVPVQPEQLASAGFYVGRNDDVKFCGCDGLRCWESGDDPWVEHAK 328
QY 61 WFFRCFL 68
Db 329 WFFRCFL 336

RESULT 2

B1R2_HUMAN STANDARD; PRT; 618 AA.
ID B1R2_HUMAN
AC Q13450; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)
 DT Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
 DE protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
 DE protein 2) (IAP homolog B).
 GN Name=BIRC2; Synonyms=API1, IAP2, MIHB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=96128127; PubMed=8549810;
 RX "The TNFR2-TRAF signaling complex contains two novel proteins related
 RT to baculoviral inhibitor of apoptosis proteins.";
 RL Cell 83:1243-1252(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RA "Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes";
 RL Nature 379:349-353(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=96209843; PubMed=8643514;
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
 RA "Cloning and expression of apoptosis inhibitory protein homologs that
 RT function to inhibit apoptosis and/or bind tumor necrosis factor
 RT receptor-associated factors";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Festis, and Uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP STRUCTURE BY NMR OF 266-363.
 RX MEDLINE=99332054; PubMed=10404221;
 RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
 RA "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
 RT repeat";
 RL Nat. Struct. Biol. 6:648-651(1999).
 CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
 CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
 CC form an heteromeric complex, which is then recruited to the tumor
 CC necrosis factor receptor 2 (TNFR2).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- TISSUE SPECIFICITY: Present in many fetal and adult tissues.

Mainly expressed in adult skeletal muscle, thymus, testis, ovary,
 and pancreas, low or absent in brain and peripheral blood
 leukocytes
 -1- SIMILARITY: Belongs to the IAP family.
 -1- SIMILARITY: Contains 3 BIR repeats.
 -1- SIMILARITY: Contains 1 CARD domain.
 -1- SIMILARITY: Contains 1 RING-type zinc finger.
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EMBL; L49431; AAC1942.1; -;
 EMBL; U45879; AAC50372.1; -;
 EMBL; U37547; AAC50508.1; -;
 EMBL; BC016174; AAH16174.1; -;
 EMBL; BC028578; AAH28578.1; -;
 PIR; S68450; S68450.
 PDB; 1QBH; NMR; A=263-363.
 Genew; HGNC:590; BIRC2.
 MIM; 601712; -;
 GO; GO:0004871; P:signal transducer activity; IEP.
 GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; TAS.
 GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . ; IEP.
 InterPro; IPR001370; BIR.
 InterPro; IPR001315; CARD.
 InterPro; IPR011029; DEATH_like.
 InterPro; IPR001841; Znf_ring.
 Pfam; PF00653; BIR; 3.
 Pfam; PF00619; CARD; 1.
 Pfam; PF00097; zf-C3HC4; 1.
 SMART; SM00238; BIR; 3.
 SMART; SM00114; CARD; 1.
 SMART; SM00184; RING; 1.
 PROSITE; PS01282; BIR_REPEAT_1; 3.
 PROSITE; PS0143; BIR_REPEAT_2; 3.
 PROSITE; PS0209; CARD; 1.
 PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 PROSITE; PS00089; ZF_RING_2; 1.
 3D-structure; Apoptosis; Repeat; Zinc-finger.
 REPEAT 46 113 BIR 1.
 REPEAT 184 250 BIR 2.
 REPEAT 269 336 BIR 3.
 DOMAIN 453 543 CARD.
 ZN_FING 571 606 RING-type.
 FT CONFLICT 157 157 S -> P (in Ref. 2).
 FT CONFLICT 308 308 C -> G (in Ref. 2).
 FT CONFLICT 414 414 Q -> L (in Ref. 2).
 FT CONFLICT 514 514 L -> W (in Ref. 2).
 FT TURN 269 270
 FT HELIX 271 274
 FT TURN 287 293
 FT TURN 294 294
 FT TURN 296 297
 FT TURN 301 304
 FT TURN 309 309
 FT STRAND 322 325
 FT HELIX 326 328
 FT TURN 333 333
 FT STRAND 334 343
 FT TURN 344 351
 FT HELIX 353 354
 FT TURN 353 354
 SQ SEQUENCE 618 AA; 69899 MW; C1778DD328063586D CRC64;
 Query Match 97.8%; Score 393; DB 1; Length 618;
 Best Local Similarity 98.5%; Pred. No. 1.5e-37;
 Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 HAAMRTFMVPSVFPVQPEQLASAGFYVGRNDDVKCFGCDGLRCWESGDDPWEHAK 60

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Db 269 HAARMRTFMWSSVPVQPEQLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVEHAK 328
Qy 61 WFPRCFEL 68
Db 329 WFPRCFEL 336

RESULT 3
BIR2_MOUSE
ID BIR2_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; C08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 2) (MIAP2) (MIAP-2).
GN Name=Birc2; Synonyms=Birc3, Iap2;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252 (1995).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.";
RL Genomics 46:495-503 (1997).
CC -!- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
CC form an heteromeric complex, which is then recruited to the tumor
CC necrosis factor receptor 2 (TNFR2).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
CC liver, skeletal muscle, kidney and testis.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; L49433; AAC42078.1; -
CC HSPB; U88909; AAC53532.1; -
CC HSPB; Q13490; IQBH.
CC MGD; MG1:1197009; Birc3.
CC GO; GO:0005515; F:protein binding; IPI.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR011029; DEATH like.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00114; CARD; 1.

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DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00083; ZF_RING_2; 1.
KW Apoptosis; Direct protein sequencing; Repeat; Zinc-finger.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-type.
FT CONFLICT 380 380 E -> K (in Ref. 2).
SQ SEQUENCE 612 AA; E08969D93C6C610D CRC64;

Query Match 91.0%; Score 366; DB 1; Length 612;
Best Local Similarity 88.2%; Pred. No. 2,3e-34;
Matches 60; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 HAARMRTFMWSSVPVQPEQLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVEHAK 60
Db 262 HSARLRTFLYWPSPVPVQPEQLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVEHAK 321
QY 61 WFPRCFEL 68
Db 322 WFPRCFEL 329

RESULT 4
Q6P6S1
ID Q6P6S1 PRELIMINARY; PRT; 589 AA.
AC Q6P6S1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Apoptosis inhibitor 2.
GN Name=Api2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.U., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC EMBL; BCC62055; AAH62055.1; -
CC InterPro; IPR001370; BIR.

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DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 589 AA; 66846 MW; 526ECBAA9052EF49 CRC64;

Query Match 89.3%; Score 359; DB 2; Length 589;
Best Local Similarity 88.2%; Pred. No. 1.4e-33;
Matches 60; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HAARMRTFMYWPSVVPQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVIEHAK 60
Db 241 HSARMSTFLYWPSSVLVQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVIEHAK 300

Qy 61 WFPCEFL 68
Db 301 WFPCEFL 308

RESULT 5
ID AAH62055 PRELIMINARY; PRT; 589 AA.
AC AAH62055;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Apoptosis inhibitor 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.U., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RC Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062055; AAH62055.1; -.
SQ SEQUENCE 589 AA; 66846 MW; 526ECBAA9052EF49 CRC64;

Query Match 89.3%; Score 359; DB 2; Length 589;
Best Local Similarity 88.2%; Pred. No. 1.4e-33;
Matches 60; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HAARMRTFMYWPSVVPQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVIEHAK 60
Db 241 HSARMSTFLYWPSSVLVQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVIEHAK 300

Qy 61 WFPCEFL 68
Db 301 WFPCEFL 308

RESULT 6
ID Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22020585; PubMed=12023884;
RA Dong Z., Nishiyama J., Yi X., Venkatachalam M.A., Denton M., Gu S.,
RA Li S., Qiang M.;
RT "Gene promoter of apoptosis inhibitory protein IAP2: identification of
RL enhancer elements and activation by severe hypoxia.";
RL Biochem. J. 364:413-421(2002).
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR HSP; Q13490; IQBF.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:000515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 589 AA; 66777 MW; E6812FFEB3EA34142 CRC64;

Query Match 87.8%; Score 353; DB 2; Length 589;
Best Local Similarity 86.8%; Pred. No. 7.3e-33;
Matches 59; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HAARMRTFMYWPSVVPQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVIEHAK 60
Db 241 HSARMSTFLYWPSSVLVQPEQLASAGFYVGRNDVVKFCGCGGLRCWESGDDPWVIEHAK 300

Qy 61 WFPCEFL 68
Db 301 WFPCEFL 308

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	SEQUENCE FROM N.A.	
RP	STRAIN=breed Leghorn; TISSUE=Spleen;	
RX	MEDLINE=2115806; PubMed=11261557;	
RA	Zhou H., Liu W., Lamont S.J.;	
RT	"Genetic variation among chicken lines and mammalian species in specific genes."	
RL	Poult. Sci. 80:284-288(2001).	
DR	EMBL; AF221082; AAF35319.1; -.	
DR	GO; GO:0005622; C:intracellular; IEA.	
DR	GO; GO:0006916; P:anti-apoptosis; IEA.	
DR	InterPro; IPR001370; BIR.	
DR	pfam; PF00653; BIR; 2.	
DR	SMART; SM00238; BIR; 2.	
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.	
DR	PROSITE; PS50143; BIR_REPEAT_2; 2.	
FT	NON TER 1	
FT	NON TER 195	
SQ	SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;	
	Query Match 87.3%; Score 351; DB 2; Length 195;	
	Best Local Similarity 82.4%; Pred.No.3.9e-33;	
	Matches 56; Conservative 7; Mismatches 5; Indels 0; Gaps 0;	
Qy	1 HAARMRTFMWPSVPVQPQLASAGFYVGRRNDVKFCDCGGLRCWESGDPPWEHAK 60 ::: ::: ::: ::: :: :: Dd 116 HEARVKTINFWTRIPVOPEQLADAGFYVGRRNDVKFCDCGGLRCWESGDPPWEHAK 175 :	
Qy	61 WFPRCFL 68 :	
Dd	176 WFPRCYL 183 :	
RESULT 9		
Q9IA69	PRELIMINARY; PRt; 197 AA.	
ID	Q9IA69 PRELIMINARY; PRt; 197 AA.	
AC	Q9IA69;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DD	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DB	Inhibitor of apoptosis 1 (fragment).	
OS	Gallus gallus (Chicken).	
OC	Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianinae;	
OC	Gallus.	
Ox	NCBI_TaxID=9031;	
EN	[1]	
RE	SEQUENCE FROM N.A.	
RP	STRAIN=breed Fayoumi; TISSUE=Spleen;	
RX	MEDLINE=2115806; PubMed=11261557;	
RA	Zhou H., Liu W., Lamont S.J.;	
RT	"Genetic variation among chicken lines and mammalian species in specific genes;"	
RL	Poult. Sci. 80:284-288(2001).	
DR	EMBL; AF221083; AAF35320.1; -.	
DR	GO; GO:0005622; C:intracellular; IEA.	
DR	GO; GO:0006916; P:anti-apoptosis; IEA.	
DR	InterPro; IPR001370; BIR.	
DR	pfaM; PF00653; BIR; 2.	
DR	SMART; SM00238; BIR; 2.	
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.	
DR	PROSITE; PS50143; BIR_REPEAT_2; 2. I	
FT	NON TER 1	
FT	NON TER 197	
SQ	SEQUENCE 197 AA; 22602 MW; D7923DACF623E1A CRC64;	
	Query Match 87.3%; Score 351; DB 2; Length 197;	
	Best Local Similarity 82.4%; Pred.No.3.9e-33;	
	Matches 56; Conservative 7; Mismatches 5; Indels 0; Gaps 0;	
Qy	1 HAARMRTFMWPSVPVQPQLASAGFYVGRRNDVKFCDCGGLRCWESGDPPWEHAK 60 ::: ::: ::: ::: :: : Db 117 HEARVKTINFWTRIPVOPEQLADAGFYVGRRNDVKFCDCGGLRCWESGDPPWEHAK 175 :	

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QY 61 WPRCEFL 68
DB 177 WPRCEYL 184

RESULT 10
BIR_CHICK
ID BIR_CHICK STANDARD; PRT; 611 AA.
AC Q90660; OS7319;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
protein).
GN Name=ITA; Synonyms=IAP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97101112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homologue of IAP that is expressed in T
lymphocytes."
RL DNA Cell Biol. 15:981-988(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Embryonic fibroblast;
RX MEDLINE=98038601; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
mediator of the antiapoptotic activity of the v-Rel oncoprotein."
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -!- FUNCTION: Apoptotic suppressor.
CC -!- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic according
to Ref.2.
CC -!- TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in
both cortical and medullary cells of the thymus. Expressed at
relatively high levels also in spleen, bursa, intestine and lung
and at very low levels in testis, brain and skeletal muscle.
CC -!- INDUCTION: High levels are induced within 4-8 hours of T-cell
activation in spleen and thymus.
CC -!- DOMAIN: The ring finger is important for its antiapoptotic effect.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U27466; AAB48118.1; --
CC DR EMBL; AF008592; AAB88044.1; --
CC DR HSP; Q33490; IQBH.
CC DR InterPro; IPR001370; BIR.
CC DR InterPro; IPR001315; CARD.
CC DR InterPro; IPR011029; DEATH_like.
CC DR InterPro; IPR001841; Znf_ring.
CC DR Pfam; PF00653; BIR; 3.
CC DR Pfam; PF00619; CARD; 1.
CC DR Pfam; PF00097; zf-C3HC4; 1.
CC DR PROSITE; PS01282; BIR_REPEAT_1; 3.
CC DR PROSITE; PS0143; BIR_REPEAT_2; 3.
CC DR PROSITE; PS02029; CARD; 1.
CC DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Nuclear protein; Repeat; Zinc-finger.
FT REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 446 536 CARD.
FT ZN_FING 564 599 RING-type.
FT CONFLICT 27 27 F -> L (in Ref. 2).
FT CONFLICT 150 150 R -> Q (in Ref. 2).
FT CONFLICT 169 169 Q -> H (in Ref. 2).
FT CONFLICT 183 183 S -> F (in Ref. 2).
FT CONFLICT 190 192 CLW -> FLS (in Ref. 2).
FT CONFLICT 196 196 V -> L (in Ref. 2).
FT CONFLICT 202 203 DD -> YY (in Ref. 2).
FT CONFLICT 213 214 VN -> FT (in Ref. 2).
FT CONFLICT 217 218 VK -> GQ (in Ref. 2).
FT CONFLICT 350 355 WNSCT -> EQLIS (in Ref. 2).
FT CONFLICT 359 359 K -> T (in Ref. 2).
FT CONFLICT 426 426 E -> D (in Ref. 2).
FT CONFLICT 492 492 T -> K (in Ref. 2).
FT CONFLICT 497 497 S -> L (in Ref. 2).
FT CONFLICT 524 524 F -> C (in Ref. 2).
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 87.3%; Score 351; DB 1; Length 611;
Best Local Similarity 82.4%; Pred. No. 1.3e-32;
Matches 56; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HAARMRTFWYWPSSVPVQPEQLASAGFYVGVGRNDVVKFCGGDLRCWESGDDPWVEHAK 60
DB 262 HEARKVTFINNPTRIPTVQPEQLADAGFYVGVGRNDVVKFCGGDLRCWESGDDPWVEHAK 321
QY 61 WPRCEFL 68
DB 322 WPRCEYL 329

RESULT 11
PIAP_PIG STANDARD; PRT; 358 AA.
AC O62640;
DT 15-DEC-1998 (Rel. 37; Created)
DT 15-DEC-1998 (Rel. 37; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Putative inhibitor of apoptosis.
GN Name=PIAP; (Pig).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98162622; PubMed=9501011;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis protein
(iap) family member is regulated by NF-kappa B."
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U79142; AAC39171.1; --
CC DR EMBL; JCS964; JCS964.

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CC or send an email to license@ib-sib.ch).
CC -----
CC EMBL; L49432; AAC41943.1; -
CC DR EMBL; U45878; AAC50371.1; -
CC DR EMBL; U37546; AAC50507.1; -
CC DR EMBL; AF070674; AAC83232.1; -
CC DR EMBL; BC037420; AAH37420.1; -
CC DR EMBL; AF178945; AAG09369.1; -
CC DR HSSP; S68449; S68449.
CC DR Genew; Q13490; 1QBH.
CC DR MIM; 601721; -.
CC DR GO; GO:0005515; F:protein binding; NAS.
CC DR GO; GO:0006916; P:anti-apoptosis; TAS.
CC DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC DR InterPro; IPR001370; BIR.
CC DR InterPro; IPR001315; CARD.
CC DR InterPro; IPR011029; DEATH like.
CC DR InterPro; IPR001841; Znf_ring.
CC DR Pfam; PF00653; BIR; 3.
CC DR Pfam; PF00619; CARD; 1.
CC DR Pfam; PF00097; zf-C3HC4; 1.
CC DR SMART; SM00238; BIR; 3.
CC DR SMART; SM00114; CARD; 1.
CC DR SMART; SM00184; RING; 1.
CC DR PROSITE; PS01282; BIR REPEAT 1; 3.
CC DR PROSITE; PS0143; BIR REPEAT 2; 3.
CC DR PROSITE; PS01039; CARD; 1.
CC DR PROSITE; PS00518; ZF RING 1; FALSE_NEG.
CC DR PROSITE; PS00089; ZF RING 2; 1.
CC KW Apoptosis; Chromosomal translocation; Repeat; Zinc-finger.
CC FT REPEAT 29 96 BIR 1.
CC FT REPEAT 169 235 BIR 2.
CC FT REPEAT 255 322 BIR 3.
CC FT DOMAIN 439 529 CARD.
CC FT ZN RING 557 592 RING-type.
CC FT SITE 442 443 BREAKPOINT FOR TRANSLOCATION TO FORM
CC FT BIRC3-MALT1.
CC FT N -> Y (in Ref. 4).
CC FT N -> H (in Ref. 2).
CC FT D -> E (in Ref. 2).
CC FT H -> P (in Ref. 2).
CC FT A -> P (in Ref. 2).
CC FT K -> R (in Ref. 2).
CC FT F -> L (in Ref. 2).
CC FT Q -> P (in Ref. 2).
CC SQ SEQUENCE 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;
CC Query Match 84.6%; Score 340; DB 1; Length 604;
CC Best Local Similarity 83.8%; Pred. No. 2.5e-31; Mismatches 4; Indels 0; Gaps 0;
CC Matches 57; Conservative 4;
CC QY 1 HAARMTFWYPSVPVQPEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAK 60
CC Db 255 HAARFKTFVFNWSSVLNVEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVQHA 314
CC QY 61 WPRCEFL 68
CC Db 315 WPRCEYL 322
CC RESULT 13
CC Q6DDY3 PRELIMINARY; PRT; 604 AA.
CC ID Q6DDY3
CC AC Q6DDY3;
CC DT 01-OCT-2004 (TrEMBLrel. 28, Created)
CC DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
CC DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CC DE Hypothetical protein.
CC OS Xenopus laevis (African clawed frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
CC OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC PubMed=12477932;
RX Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.I., Marra M.A.;
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC077368; AAH77368.1; -.
SQ SEQUENCE 604 AA; 68551 MW; 78B5CC51E111CC84 CRC64;
Query Match 83.1%; Score 334; DB 2; Length 604;
Best Local Similarity 80.6%; Pred. No. 1.3e-30;
Matches 54; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 2 AARMTFWYPSVPVQPEQLASAGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAKW 61
Db 257 SARLKTFFVSWPPRIPVPTQLAAGFYVGRNDVKFCGDCGLRCWESGDDPWVEHAKW 316
QY 62 FPRCEFL 68
Db 317 FPRCEYL 323
RESULT 14
Q8UWD2 PRELIMINARY; PRT; 628 AA.
ID Q8UWD2
AC Q8UWD2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Iap1.
GN Names-birc3; Synonyms-iap1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CC NCBI_TaxID=7955;
RN SEQUENCE FROM N.A.
RP MEDLINE=20373792; PubMed=10917738;
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